



#10

1

# SEQUENCE LISTING

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<120> Cone Snail Peptides

<130> 2314-249

<150> US 60/267,408

<151> 2001-02-09

<160> 638

<170> PatentIn version 3.0

<210> 1

<211> 290

<212> DNA

<213> Conus ammiralis

<220>

<221> CDS

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Met Glu Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met	
1 5 10 15	

tgc acc cag gcc ctg gtt gaa cgt gct gga gaa aac cgc tca aag gag	96
Ser Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn Arg Ser Lys Glu	
20 25 30	

aac atc aat ttt tta tta aaa aga aag aga gct gct gac agg ggg atg	144
Asn Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met	
35 40 45	

tgg ggc gat tgc aaa gat ggg tta acg aca tgt ttt gcg ccc tca gag	192
Trp Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro Ser Glu	
50 55 60	

tgt tgt tct gag gat tgt gaa ggg agc tgc acg atg tgg tgatgacctc	241
Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp	
65 70 75	

tgaccacaag ccattctgaca tcaccactct cctcttcaga ggcttcaag	290
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<210> 2

<211> 76

<212> PRT

<213> Conus ammiralis

<400> 2

Met Glu Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15

Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn Arg Ser Lys Glu Asn  
20 25 30

Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp  
35 40 45

Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro Ser Glu Cys  
50 55 60

Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp  
65 70 75

<210> 3

<211> 31

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residues 18, 22 and 25 is Glu or gamma-carboxy-Glu;  
Xaa at residue 16 is Pro or hydroxy-Pro; Xaa at residues 3  
and 31 is Trp (D or L) or bromo-Trp (D or L)

<400> 3

Gly Met Xaa Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Xaa  
1 5 10 15

Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa  
20 25 30

<210> 4

<211> 295

<212> DNA

<213> Conus ammiralis

<220>

<221> CDS

<222> (4)..(246)

<400> 4

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Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met  
1 5 10 15

tcg acc cag gcc ctg cct caa ggt ggt gga gaa aaa cgc cca agg gag 96  
Ser Thr Gln Ala Leu Pro Gln Gly Gly Gly Glu Lys Arg Pro Arg Glu  
20 25 30

aat atc aga ttt tta tca aaa aga aag aca aat gct gag cgt tgg agg 144  
Asn Ile Arg Phe Leu Ser Lys Arg Lys Thr Asn Ala Glu Arg Trp Arg  
35 40 45

gag ggc agt tgc acc tct tgg tta gcg acg tgt acg caa gac cag caa 192  
 Glu Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp Gln Gln  
           50                          55                          60

tgc tgt act gat gtt tgt tac aaa agg gac tac tgc gcc ttg tgg gat 240  
 Cys Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu Trp Asp  
           65                          70                          75

gac cgc tgaccacaag ccattctgaca tcaccactct cctgttcaga gtcttcaag 295  
 Asp Arg  
 80

<210> 5  
 <211> 81  
 <212> PRT  
 <213> Conus ammiralis

<400> 5  
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 1                          5                          10                          15

Thr Gln Ala Leu Pro Gln Gly Gly Gly Glu Lys Arg Pro Arg Glu Asn  
           20                          25                          30

Ile Arg Phe Leu Ser Lys Arg Lys Thr Asn Ala Glu Arg Trp Arg Glu  
           35                          40                          45

Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp Gln Gln Cys  
           50                          55                          60

Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu Trp Asp Asp  
           65                          70                          75                          80

Arg

<210> 6  
 <211> 36  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at  
       residues 1, 9 and 33 is Trp (D or L) or bromo-Trp  
       (D or L); Xaa at residues 25 and 29 is Tyr, 125I-Tyr,  
       mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 6  
 Xaa Arg Xaa Gly Ser Cys Thr Ser Xaa Leu Ala Thr Cys Thr Gln Asp  
 1                          5                          10                          15

Gln Gln Cys Cys Thr Asp Val Cys Xaa Lys Arg Asp Xaa Cys Ala Leu  
           20                          25                          30

Xaa Asp Asp Arg  
           35

<210> 7  
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<212> DNA  
 <213> *Conus ammiralis*

<220>  
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 <222> (4)..(219)

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     1                  5                  10                  15  
  
 tcg acc cag gcc ctg ttt caa gaa aaa cgc aca atg aag aag atc gat 96  
 Ser Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp  
                   20                  25                  30  
  
 ttt tta tca aag gga aag gca gat gct gag aag cag agg aag cgc aat 144  
 Phe Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn  
                   35                  40                  45  
  
 tgc tcg gat gat tgg cag tat tgt gaa agt ccc agt gac tgc tgt agt 192  
 Cys Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser  
           50                  55                  60  
  
 tgg gat tgt gat gtg gtc tgc tcg gga tgaactctga ccacaagtca 239  
 Trp Asp Cys Asp Val Val Cys Ser Gly  
   65                  70  
  
 tccgacatca ccactctcct gttcagaggc ttcaag 275

<210> 8  
 <211> 72  
 <212> PRT  
 <213> *Conus ammiralis*

<400> 8  
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
 1                  5                  10                  15  
  
 Thr Gln Ala Leu Phe Gln Glu Lys Arg Thr Met Lys Lys Ile Asp Phe  
                   20                  25                  30  
  
 Leu Ser Lys Gly Lys Ala Asp Ala Glu Lys Gln Arg Lys Arg Asn Cys  
           35                  40                  45  
  
 Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys Ser Trp  
   50                  55                  60  
  
 Asp Cys Asp Val Val Cys Ser Gly  
 65                  70

<210> 9  
 <211> 25  
 <212> PRT  
 <213> *Conus ammiralis*

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residue 12



is Pro or hydroxy-Pro; Xaa at residues 6 and 18 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 9

Asn Cys Ser Asp Asp Xaa Gln Xaa Cys Xaa Ser Xaa Ser Asp Cys Cys  
1 5 10 15

Ser Xaa Asp Cys Asp Val Val Cys Ser  
20 25

<210> 10

<211> 280

<212> DNA

<213> *Conus ammiralis*

<220>

<221> CDS

<222> (4)..(246)

<400> 10

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Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Leu Leu Leu  
1 5 10 15

tcg atc cag gcg gta aat caa gaa aaa cac caa cgg gca aag atc aac 96  
Ser Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn  
20 25 30

ttg ctt tca aag aga aag cca cct gct gag cgt tgg tgg cgg tgg gga 144  
Leu Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly  
35 40 45

gga tgc atg gct tgg ttt ggg aaa tgt tcg aag gac tcg gaa tgt tgt 192  
Gly Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys  
50 55 60

tct aat agt tgt gac ata acg cgc tgc gag tta atg cga ttc cca cca 240  
Ser Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro  
65 70 75

gac tgg tgacatcgac actctcctgt tcagagtctt caag 280  
Asp Trp  
80

<210> 11

<211> 81

<212> PRT

<213> *Conus ammiralis*

<400> 11

Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Leu Leu Leu Ser  
1 5 10 15

Ile Gln Ala Val Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu  
20 25 30

Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly  
35 40 45

Cys Met Ala Trp Phe Gly Lys Cys Ser Lys Asp Ser Glu Cys Cys Ser  
50 55 60

Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu Met Arg Phe Pro Pro Asp  
65 70 75 80  
Trp

<210> 12  
<211> 39  
<212> PRT  
<213> Conus ammiralis

<220>  
<221> PEPTIDE  
<222> (1)..(39)  
<223> Xaa at residues 19 and 31 is Glu or gamma-carboxy-Glu; Xaa at  
residues 36 and 37 is Pro or hydroxy-Pro; Xaa at residues 1, 2,  
4, 10 and 39 is Trp (D or L) or bromo-Trp (D or L)

<400> 12  
Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Lys Cys Ser Lys  
1 5 10 15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Ile Thr Arg Cys Xaa Leu  
20 25 30

Met Arg Phe Xaa Xaa Asp Xaa  
35

<210> 13  
<211> 267  
<212> DNA  
<213> Conus ammiralis

<220>  
<221> CDS  
<222> (4)..(213)

<400> 13  
atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg acg 48  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Thr  
1 5 10 15

tcg acc cag gcc ctg att caa ggt ggt gga gac gaa cgc caa aag gca 96  
Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Asp Glu Arg Gln Lys Ala  
20 25 30

aag atc aac ttt ctt tca agg tcg gac cgc gat tgc agg ggt tac gat 144  
Lys Ile Asn Phe Leu Ser Arg Ser Asp Arg Asp Cys Arg Gly Tyr Asp  
35 40 45

gcg ccg tgt agc tct ggc gcg cca tgt tgt gat tgg tgg aca tgt tca 192  
Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys Asp Trp Trp Thr Cys Ser  
50 55 60

gca cga acc ggg cgc tgt ttt taggctgacc acaagccatc cgacatcacc 243  
Ala Arg Thr Gly Arg Cys Phe  
65 70

actctcctct tcagaggctt caag 267

<210> 14  
 <211> 70  
 <212> PRT  
 <213> *Conus ammiralis*

<400> 14  
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Thr Ser  
 1 5 10 15  
 Thr Gln Ala Leu Ile Gln Gly Gly Gly Asp Glu Arg Gln Lys Ala Lys  
 20 25 30  
 Ile Asn Phe Leu Ser Arg Ser Asp Arg Asp Cys Arg Gly Tyr Asp Ala  
 35 40 45  
 Pro Cys Ser Ser Gly Ala Pro Cys Cys Asp Trp Trp Thr Cys Ser Ala  
 50 55 60  
 Arg Thr Gly Arg Cys Phe  
 65 70

<210> 15  
 <211> 29  
 <212> PRT  
 <213> *Conus ammiralis*

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residues 8 and 14 is Pro or hydroxy-Pro; Xaa at residues  
 18 and 19 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue  
 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 15  
 Asp Cys Arg Gly Xaa Asp Ala Xaa Cys Ser Ser Gly Ala Xaa Cys Cys  
 1 5 10 15  
 Asp Xaa Xaa Thr Cys Ser Ala Arg Thr Gly Arg Cys Phe  
 20 25

<210> 16  
 <211> 277  
 <212> DNA  
 <213> *Conus ammiralis*

<220>  
 <221> CDS  
 <222> (4)..(222)

<400> 16  
 atc atg cag aaa ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg 48  
 Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met  
 1 5 10 15  
 tcg acc cag gcc gtg ctt caa gaa aaa cgc cca aag gag aag atc aag 96  
 Ser Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys  
 20 25 30

ttt tta tca aag aaa aag aca gat gct gag aag cag cag aag cgc ctt 144  
 Phe Leu Ser Lys Lys Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu  
           35                  40                  45

tgc ccg gat tac acg gag cct tgt tca cat gcc cat gaa tgc tgt tca 192  
 Cys Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser  
           50                  55                  60

tgg aat tgt cat aat ggg cac tgc acg gga tgaactcgga ccacaagcca 242  
 Trp Asn Cys His Asn Gly His Cys Thr Gly  
           65                  70

tcgacatcat cactctcctg ttcagagtct tcaag 277

<210> 17  
 <211> 73  
 <212> PRT  
 <213> Conus ammiralis

<400> 17  
 Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
 1                  5                  10                  15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Phe  
           20                  25                  30

Leu Ser Lys Lys Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys  
           35                  40                  45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp  
           50                  55                  60

Asn Cys His Asn Gly His Cys Thr Gly  
 65                  70

<210> 18  
 <211> 26  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residues 7 and 14 is Glu or gamma-carboxy-Glu; Xaa at  
 residues 3 and 8 is Pro or hydroxy-Pro; Xaa at residue 18 is Trp  
 (D or L) or bromo-Trp (D or L); Xaa at residue 5 is Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 18  
 Leu Cys Xaa Asp Xaa Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys  
 1                  5                  10                  15

Ser Xaa Asn Cys His Asn Gly His Cys Thr  
           20                  25

<210> 19  
 <211> 287  
 <212> DNA  
 <213> Conus ammiralis

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<220>
<221> CDS
<222> (4)..(228)

<400> 19
atc atg cag aaa ctg ata att ctg ctc ctt gtt gct gct gta ctg atg      48
    Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
      1              5              10              15

tcg acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc cgg aaa gcg      96
Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala
                20              25              30

gag atc aac ttt tct aaa aca aga aat ttg gcg aga aac aag cag aaa      144
Glu Ile Asn Phe Ser Lys Thr Arg Asn Leu Ala Arg Asn Lys Gln Lys
                35              40              45

cgc tgc agt agt tgg gca aag tat tgt gaa gtt gac tcg gaa tgc tgt      192
Arg Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys
                50              55              60

tcc gaa cag tgt gta agg tct tac tgc gcg atg tgg tgatgacctc      238
Ser Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp
      65              70              75

tgaccacaag ccatccgata tcaccactct cctcttcaga gacttcaag      287

<210> 20
<211> 75
<212> PRT
<213> Conus ammiralis

<400> 20
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
1              5              10              15

Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu
      20              25              30

Ile Asn Phe Ser Lys Thr Arg Asn Leu Ala Arg Asn Lys Gln Lys Arg
      35              40              45

Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys Ser
      50              55              60

Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp
65              70              75

<210> 21
<211> 27
<212> PRT
<213> Conus ammiralis

<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 9, 13 and 17 is Glu or gamma-carboxy-Glu; Xaa at
      residue 13 is Pro or hydroxy-Pro; Xaa at residues 4 and 27 is Trp
      (D or L) or bromo-Trp (D or L);

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<220>
<221> PEPTIDE
<222> (1)..(27)
<223> Xaa at residues 7 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
      iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 21
Cys Ser Ser Xaa Ala Lys Xaa Cys Xaa Val Asp Ser Xaa Cys Cys Ser
1          5          10          15

Xaa Gln Cys Val Arg Ser Xaa Cys Ala Met Xaa
          20          25

<210> 22
<211> 461
<212> DNA
<213> Conus ammiralis

<220>
<221> CDS
<222> (4)..(270)

<400> 22
gtt aaa atg cat ctg tca ctg gca cgc tca gct gtt ttg atg ttg ctt      48
  Lys Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu
  1          5          10          15

ctg ctg ttt gcc ttg ggc aac ttt gtt gtg gtc cag tca gga cag ata      96
Leu Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile
          20          25          30

aca aga gat gtg gac aat gga cag ctc acg gac aac cgc cgt aac ctg      144
Thr Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu
          35          40          45

caa tcg aag tgg aag cca gtg agt ctc ttc atg tca cga cgg tct tgt      192
Gln Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys
          50          55          60

aac aat tct tgc aat gag cat tcc gat tgc gaa tcc cat tgt att tgc      240
Asn Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys
          65          70          75

acg ttt agc gga tgc aaa att att ttg ata taaacggatt gagtttgctc      290
Thr Phe Ser Gly Cys Lys Ile Ile Leu Ile
80          85

gtcaacaaga tgtcgcaacta cagctcctct ctacagtgtg tacatcgacc aaacgacgca      350

tctttttatatt ctttgtctgt tgtatttggt ttctgtgtt cataacgtac agagcccttt      410

aattaccttt actgctcttc acttaacctg ataaccggaa ggtccagtgc t      461

<210> 23
<211> 89
<212> PRT
<213> Conus ammiralis

<400> 23
Lys Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu

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1                      5                      10                      15  
 Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile Thr  
                     20                      25                      30  
 Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu Gln  
                     35                      40                      45  
 Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys Asn  
                     50                      55                      60  
 Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys Thr  
                     65                      70                      75                      80  
 Phe Ser Gly Cys Lys Ile Ile Leu Ile  
                     85

<210> 24  
 <211> 28  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu

<400> 24  
 Ser Cys Asn Asn Ser Cys Asn Xaa His Ser Asp Cys Xaa Ser His Cys  
 1                      5                      10                      15

Ile Cys Thr Phe Ser Gly Cys Lys Ile Ile Leu Ile  
                     20                      25

<210> 25  
 <211> 459  
 <212> DNA  
 <213> Conus ammiralis

<220>  
 <221> CDS  
 <222> (7)..(270)

<400> 25  
 gttaaa atg cat ctg tca ctg gca cgc tta gct gtt ttg atg ttg ctt                      48  
          Met His Leu Ser Leu Ala Arg Leu Ala Val Leu Met Leu Leu  
          1                      5                      10  
  
 ctg ctg ttt gcc ttg ggc aac ttt gtt gtg gtc cag tca gga cag ata                      96  
 Leu Leu Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile  
 15                      20                      25                      30  
  
 aca aga gat gtg gac aat gga cag ctc acg gac aac cgc cgt aac ctg                      144  
 Thr Arg Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu  
                     35                      40                      45  
  
 caa tcg aag tgg aag cca gtg agt ctc ttc atg tca cga cgg tct tgt                      192  
 Gln Ser Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys  
                     50                      55                      60

aac aat tct tgc aat gag cat tcc gat tgc gaa tcc cat tgt att tgc 240  
 Asn Asn Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys  
           65                              70                              75                              .

acg ttt aga gga tgc gga gct gtt aat ggt tgagtttgct cgtcaacatg 290  
 Thr Phe Arg Gly Cys Gly Ala Val Asn Gly  
           80                              85

atgtcgcaact acacactaca gctcctctct acagtgtgta catcgaccaa acgacgcac 350

ttttattttct ttgtctgttg tgtttgtttt cctgtgttca taacgtacag agccctttaa 410

ttactttttac tgctcttcac ttaacctgat aaccagaagg tccagtgtc 459

<210> 26

<211> 88

<212> PRT

<213> Conus ammiralis

<400> 26

Met His Leu Ser Leu Ala Arg Leu Ala Val Leu Met Leu Leu Leu Leu  
 1                              5                              10                              15

Phe Ala Leu Gly Asn Phe Val Val Val Gln Ser Gly Gln Ile Thr Arg  
           20                              25                              30

Asp Val Asp Asn Gly Gln Leu Thr Asp Asn Arg Arg Asn Leu Gln Ser  
           35                              40                              45

Lys Trp Lys Pro Val Ser Leu Phe Met Ser Arg Arg Ser Cys Asn Asn  
           50                              55                              60

Ser Cys Asn Glu His Ser Asp Cys Glu Ser His Cys Ile Cys Thr Phe  
 65                              70                              75                              80

Arg Gly Cys Gly Ala Val Asn Gly  
                               85

<210> 27

<211> 27

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 8 and 13 is Glu or gamma-carboxy-Glu

<400> 27

Ser Cys Asn Asn Ser Cys Asn Xaa His Ser Asp Cys Xaa Ser His Cys  
 1                              5                              10                              15

Ile Cys Thr Phe Arg Gly Cys Gly Ala Val Asn  
           20                              25

<210> 28

<211> 387

<212> DNA

<213> Conus arenatus



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (19)..(240)

&lt;400&gt; 28

accaaaacca tcatcaaa atg aaa ctg acg tgc gtg gtg atc gtc gct gtg 51  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val  
 1 5 10

ctg ttc ctg acg gcc tgt caa ctc act aca gct gat gac tcc aga ggt 99  
 Leu Phe Leu Thr Ala Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly  
 15 20 25

acg cag aag cat ggt gcc ctg aga tcg acc acc aaa ctc tcc atg ttg 147  
 Thr Gln Lys His Gly Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu  
 30 35 40

act cgg ggc tgc acg cct cct ggt gga gtt tgt ggt tat cat ggt cac 195  
 Thr Arg Gly Cys Thr Pro Pro Gly Gly Val Cys Gly Tyr His Gly His  
 45 50 55

tgc tgc gat ttt tgc gat acg ttc ggc aat tta tgt gtg agt ggc 240  
 Cys Cys Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser Gly  
 60 65 70

tgacccggca tctgaccttt ccccttcttt tgctccacta tcctttttct gcctgagtcc 300

tccataacctg agagctgtca tgaaccactc aacacctact cttccggagg tttctgagga 360

gctgcattga aataaaagcc gcattgac 387

&lt;210&gt; 29

&lt;211&gt; 74

&lt;212&gt; PRT

&lt;213&gt; Conus arenatus

&lt;400&gt; 29

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Thr Thr Ala Asp Asp Ser Arg Gly Thr Gln Lys His Gly  
 20 25 30

Ala Leu Arg Ser Thr Thr Lys Leu Ser Met Leu Thr Arg Gly Cys Thr  
 35 40 45

Pro Pro Gly Gly Val Cys Gly Tyr His Gly His Cys Cys Asp Phe Cys  
 50 55 60

Asp Thr Phe Gly Asn Leu Cys Val Ser Gly  
 65 70

&lt;210&gt; 30

&lt;211&gt; 28

&lt;212&gt; PRT

&lt;213&gt; Conus arenatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(28)

<223> Xaa at residues 4 and 5 is Pro or hydroxy-Pro; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 30

Gly Cys Thr Xaa Xaa Gly Gly Val Cys Gly Xaa His Gly His Cys Cys  
1 5 10 15

Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser  
20 25

<210> 31

<211> 375

<212> DNA

<213> *Conus arenatus*

<220>

<221> CDS

<222> (24)..(260)

<400> 31

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53  
Met Ser Gly Leu Gly Ile Met Val Leu Thr  
1 5 10

ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101  
Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu  
15 20 25

aag aag gcg atg caa agg gac gca atc aac gtc aga cgg aga aga tca 149  
Lys Lys Ala Met Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser  
30 35 40

ctc act cgg gga gta gta act gag gcg tgc gaa gag tcc tgt gag gag 197  
Leu Thr Arg Gly Val Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu  
45 50 55

gag gaa aag cac tgc tgc cac gta aat aat gga gta ccc tct tgt gcc 245  
Glu Glu Lys His Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala  
60 65 70

gtt ata tgc tgg gga tagtttctcg cacactgtct cattcattat tttatcagta 300  
Val Ile Cys Trp Gly  
75

caagtgtaaa cgagacatgt cagaaagtcg aaggttgtgc gtatttgata agtattgttt 360

actgggatga acgga 375

<210> 32

<211> 79

<212> PRT

<213> *Conus arenatus*

<400> 32

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe  
1 5 10 15

Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Lys Ala Met Gln Arg  
20 25 30

Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Leu Thr Arg Gly Val Val  
                   35                                  40                                  45

Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu Glu Glu Lys His Cys Cys  
           50                                  55                                  60

His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp Gly  
   65                                  70                                  75

<210> 33

<211> 32

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 4, 7, 8, 11, 12, 13 and 14 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro; Xaa at residue 32 is Trp (D or L) or bromo-Trp (D or L)

<400> 33

Val Val Thr Xaa Ala Cys Xaa Xaa Ser Cys Xaa Xaa Xaa Xaa Lys His  
   1                                  5                                  10                                  15

Cys Cys His Val Asn Asn Gly Val Xaa Ser Cys Ala Val Ile Cys Xaa  
                   20                                  25                                  30

<210> 34

<211> 375

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (24)..(260)

<400> 34

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53  
                                   Met Ser Gly Leu Gly Ile Met Val Leu Thr  
                                   1                                  5                                  10

ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101  
   Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu  
                   15                                  20                                  25

aag cag gcg acg gaa agg gac gca atc aac atc aga tgg aga aga tca 149  
   Lys Gln Ala Thr Glu Arg Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser  
                   30                                  35                                  40

cgc act cgg aga ata gta act gag gcg tgc gaa gag tcc tgt gag gac 197  
   Arg Thr Arg Arg Ile Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp  
                   45                                  50                                  55

gag gaa aag cac tgc tgc cac gta aat aat gga gta ccc tct tgt gcc 245  
   Glu Glu Lys His Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala  
                   60                                  65                                  70

gtt ata tgc tgg gga tagtttctcg cacactgtct cattcattat tttatcagta 300

Val Ile Cys Trp Gly  
75

caagtgtaaa cgagacatgt cagaaagtcg aaggttggtgc gtatttgata agtattgttt 360

actgggatga acgga 375

<210> 35  
<211> 79  
<212> PRT  
<213> Conus arenatus

<400> 35  
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe  
1 5 10 15

Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Thr Glu Arg  
20 25 30

Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser Arg Thr Arg Arg Ile Val  
35 40 45

Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp Glu Glu Lys His Cys Cys  
50 55 60

His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp Gly  
65 70 75

<210> 36  
<211> 32  
<212> PRT  
<213> Conus arenatus

<220>  
<221> PEPTIDE  
<222> (1)..(32)  
<223> Xaa at residues 4, 7, 8, 11, 13 and 14 is Glu or gamma-carboxy-  
Glu; Xaa at residue 25 is Pro or hydroxy-Pro; Xaa at residue 32  
is Trp (D or L) or bromo-Trp (D or L)

<400> 36  
Ile Val Thr Xaa Ala Cys Xaa Xaa Ser Cys Xaa Asp Xaa Xaa Lys His  
1 5 10 15

Cys Cys His Val Asn Asn Gly Val Xaa Ser Cys Ala Val Ile Cys Xaa  
20 25 30

<210> 37  
<211> 374  
<212> DNA  
<213> Conus arenatus

<220>  
<221> CDS  
<222> (24)..(260)

<400> 37  
gacaggattg aacaaaattc agg atg tca gaa ctg gga atc atg gtg cta acg 53  
Met Ser Glu Leu Gly Ile Met Val Leu Thr  
1 5 10

ctt	cta	ctt	ctt	gtg	ttc	ctg	gta	acc	agt	cat	cag	gat	gca	gga	gag	101
Leu	Leu	Leu	Leu	Val	Phe	Leu	Val	Thr	Ser	His	Gln	Asp	Ala	Gly	Glu	
				15					20					25		

aag cag gcg acg gaa agg gac gca atc aac atc aga tgg aga aga tca 149  
Lys Gln Ala Thr Glu Arg Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser  
30 35 40

ctc act cgg aga ata gta act gag gcg tgc gaa gag cac tgt gag gat 197  
Leu Thr Arg Arg Ile Val Thr Glu Ala Cys Glu Glu His Cys Glu Asp  
45 50 55

gag gaa cag ttc tgc tgc ggc tta gag aat gga caa ccc ttt tgt gcc 245  
Glu Glu Gln Phe Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala  
60 65 70

cct gtt tgc ttc gga tagtttctgt acactgtctc attaattatt ttatcagtac 300  
Pro Val Cys Phe Gly  
75

aagtgtaaac aaaacatgtc agaaagtcga aggttggtcgc tatttgataa gtattgtttg 360

ctgggacgaa cgga 374

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<210> 38
<211> 79
<212> PRT
<213> Conus arenatus
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```
<400> 38
Met Ser Glu Leu Gly Ile Met Val Leu Thr Leu Leu Leu Val Phe
1          5          10          15
```

Leu Val Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Thr Glu Arg  
20 25 30

Asp Ala Ile Asn Ile Arg Trp Arg Arg Ser Leu Thr Arg Arg Ile Val  
35 40 45

Thr Glu Ala Cys Glu Glu His Cys Glu Asp Glu Glu Gln Phe Cys Cys  
50 55 60

Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Pro Val Cys Phe Gly  
65 70 75

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<210> 39
<211> 32
<212> PRT
<213> Conus arenatus
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```
<220>
<221>    PEPTIDE
<222>    (1)..(32)
<223>    Xaa at residues 4, 7, 8, 11, 13, 14 and 21 is Glu or gamma-
carboxy-Glu; Xaa at residues 25 and 29 is Pro or hydroxy-Pro
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```
<400> 39
Ile Val Thr Xaa Ala Cys Xaa Xaa His Cys Xaa Asp Xaa Xaa Gln Phe
1          5          10          15
```

Cys Cys Gly Leu Xaa Asn Gly Gln Xaa Phe Cys Ala Xaa Val Cys Phe  
20 25 30

```
<210> 40
<211> 375
<212> DNA
<213> Conus arenatus
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<220>
<221> CDS
<222> (24) .. (260)
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<400> 40
gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53
          Met Ser Gly Leu Gly Ile Met Val Leu Thr
          1          5          10
```

ctt cta ctt ctt gtg ttc atg gca acc agt cat cag gat gca gga gag 101  
 Leu Leu Leu Leu Val Phe Met Ala Thr Ser His Gln Asp Ala Gly Glu  
 15 20 25

aag aag gtg atg caa agg gac gca atc aac gtc aga cgg aga aga tca 149  
Lys Lys Val Met Gln Arg Asp Ala Ile Asn Val Arg Arg Arg Arg Ser  
30 35 40

cgc act cgg aga gta gta act ggg gcg tgc gaa gag cac tgt gag gac 197  
 Arg Thr Arg Arg Val Val Thr Gly Ala Cys Glu Glu His Cys Glu Asp  
           45                          50                          55

gag gaa aag cac tgc tgc ggc tta gag aat gga caa ccc ttt tgt gcc 245  
Glu Glu Lys His Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala  
60 65 70

cgt cta tgc tta gga tagttttctg tacactgtct tattcattat tttatcagta 300  
Arg Leu Cys Leu Gly  
75

caagtgaaaa caaagcatgt cagaaagtcg aaggttgtgc gtatttgata agtattgttt 360

actgggatga acgga 375

<210>	41
<211>	79
<212>	PRT
<213>	Conus arenatus

<400> 41  
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Phe  
1 5 10 15

Met Ala Thr Ser His Gln Asp Ala Gly Glu Lys Lys Val Met Gln Arg  
20 25 30

Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Arg Thr Arg Arg Val Val  
35 40 45

Thr Gly Ala Cys Glu Glu His Cys Glu Asp Glu Glu Lys His Cys Cys  
50 55 60

Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Arg Leu Cys Leu Gly  
 65 70 75

<210> 42  
 <211> 32  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 7, 8, 11, 13, 14 and 21 is Glu or gamma-carboxy-Glu; Xaa at residue 25 is Pro or hydroxy-Pro

<400> 42  
 Val Val Thr Gly Ala Cys Xaa Xaa His Cys Xaa Asp Xaa Xaa Lys His  
 1 5 10 15

Cys Cys Gly Leu Xaa Asn Gly Gln Xaa Phe Cys Ala Arg Leu Cys Leu  
 20 25 30

<210> 43  
 <211> 219  
 <212> DNA  
 <213> Conus arenatus

<220>  
 <221> CDS  
 <222> (1)..(189)

<400> 43  
 atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48  
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
 1 5 10 15

acc cag gtc atg gtt caa ggt gac gga gat caa cct gca gct cgc aat 96  
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn  
 20 25 30

gca gtg cca aaa gac gat aac cca gat gga gcg agt gga aag ttc atg 144  
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met  
 35 40 45

aat gtt cta cgt cgg tct gga tgt ccg tgg cat cct tgg tgt ggc 189  
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp His Pro Trp Cys Gly  
 50 55 60

tgatcggaat ccacgattgc aatgacagcc 219

<210> 44  
 <211> 63  
 <212> PRT  
 <213> Conus arenatus

<400> 44  
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
 1 5 10 15

Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn  
 20 25 30

Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met  
           35                          40                          45

Asn Val Leu Arg Arg Ser Gly Cys Pro Trp His Pro Trp Cys Gly  
       50                          55                          60

<210> 45

<211> 9

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(9)

<223> Xaa at residues 4 and 7 is Pro or hydroxy-Pro; Xaa at residues 5  
       and 8 is Trp (D or L) or bromo-Trp (D or L)

<400> 45

Ser Gly Cys Xaa Xaa His Xaa Xaa Cys  
   1                          5

<210> 46

<211> 219

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (1)..(189)

<400> 46

atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg       48  
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
   1                          5                          10                          15

acc cag gtc atg gtt caa ggt gac gga gat caa cct gca gct cgc aat       96  
 Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn  
                           20                          25                          30

gca gtg cca aaa gac gat aac cca gat gga gcg agt gga aag ttc atg       144  
 Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met  
                           35                          40                          45

aat gtt cta cgt cgg tct gga tgt ccg tgg cgc cct tgg tgt ggc       189  
 Asn Val Leu Arg Arg Ser Gly Cys Pro Trp Arg Pro Trp Cys Gly  
       50                          55                          60

tgatcggaaat ccacgattgc aatgacagcc       219

<210> 47

<211> 63

<212> PRT

<213> Conus arenatus

<400> 47

Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
   1                          5                          10                          15

Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Ala Arg Asn



```

      20              25              30
Ala Val Pro Lys Asp Asp Asn Pro Asp Gly Ala Ser Gly Lys Phe Met
      35              40              45

Asn Val Leu Arg Arg Ser Gly Cys Pro Trp Arg Pro Trp Cys Gly
      50              55              60

<210> 48
<211> 10
<212> PRT
<213> Conus arenatus

<220>
<221> PEPTIDE
<222> (1)..(10)
<223> Xaa at residues 5 and 8 is Pro or hydroxy-Pro; Xaa at residues 6
      and 9 is Trp (D or L) or bromo-Trp (D or L)

<400> 48
Ala Ser Gly Cys Xaa Xaa Arg Xaa Xaa Cys
1              5              10

<210> 49
<211> 219
<212> DNA
<213> Conus arenatus

<220>
<221> CDS
<222> (1)..(189)

<400> 49
atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg      48
Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
1              5              10              15

acc cag gtc atg gtt caa ggt gac gga gat caa cct gca ggt cga gat      96
Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Gly Arg Asp
      20              25              30

gca gtt cca aga gac gat aac cca ggt gga acg agt gga aag ttc atg      144
Ala Val Pro Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Met
      35              40              45

aat gct cta cgt caa tat gga tgt ccg gtg ggt ctt tgg tgt gac      189
Asn Ala Leu Arg Gln Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp
      50              55              60

tgatcagaat ccacgattgc aatgacagcc      219

<210> 50
<211> 63
<212> PRT
<213> Conus arenatus

<400> 50
Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser
1              5              10              15

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Thr Gln Val Met Val Gln Gly Asp Gly Asp Gln Pro Ala Gly Arg Asp  
                   20                  25                  30

Ala Val Pro Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Met  
           35                  40                  45

Asn Ala Leu Arg Gln Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp  
       50                  55                  60

<210> 51

<211> 11

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at residue 9 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 51

Xaa Xaa Gly Cys Xaa Val Gly Leu Xaa Cys Asp  
   1                  5                  10

<210> 52

<211> 210

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (1)..(180)

<400> 52

atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg           48  
 Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
   1                  5                  10                  15

acc cag gtc atg ttt cga gat caa cct gca cgt cgt gat gca gtg cca           96  
 Thr Gln Val Met Phe Arg Asp Gln Pro Ala Arg Arg Asp Ala Val Pro  
           20                  25                  30

aga gac gat agc cca gat gga atg agt gga ggg ttc atg aat gtc cca           144  
 Arg Asp Asp Ser Pro Asp Gly Met Ser Gly Gly Phe Met Asn Val Pro  
           35                  40                  45

cgt cgg tct gga tgt ccg tgg caa cct tgg tgt ggc tgatcggaat           190  
 Arg Arg Ser Gly Cys Pro Trp Gln Pro Trp Cys Gly  
       50                  55                  60

ccacgattgc aatgacagcc   210

<210> 53

<211> 60

<212> PRT

<213> Conus arenatus

<400> 53

Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15

Thr Gln Val Met Phe Arg Asp Gln Pro Ala Arg Arg Asp Ala Val Pro  
20 25 30

Arg Asp Asp Ser Pro Asp Gly Met Ser Gly Gly Phe Met Asn Val Pro  
35 40 45

Arg Arg Ser Gly Cys Pro Trp Gln Pro Trp Cys Gly  
50 55 60

<210> 54

<211> 9

<212> PRT

<213> Conus arenatus

<220>

<221> PEPTIDE

<222> (1)..(9)

<223> Xaa at residues 4 and 7 is Pro or hydroxy-Pro; Xaa at residues 5 and 8 is Trp (D or L) or bromo-Trp (D or L)

<400> 54

Ser Gly Cys Xaa Xaa Gln Xaa Xaa Cys  
1 5

<210> 55

<211> 210

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (1)..(180)

<400> 55

atg ggg aaa ctg aca ata ctg gtt ctt gtt gct gct gta ctg ttg tcg 48  
Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15

acc cag gcc atg gtt caa gat caa cct gca ggt cga gat gca gtt cca 96  
Thr Gln Ala Met Val Gln Asp Gln Pro Ala Gly Arg Asp Ala Val Pro  
20 25 30

aga gac gat aac cca ggt gga acg agt gga aag ttc gtg aat gct caa 144  
Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Val Asn Ala Gln  
35 40 45

cgt caa tat gga tgt ccg ccg ggt ctt tgg tgt cac tgatcagaat 190  
Arg Gln Tyr Gly Cys Pro Pro Gly Leu Trp Cys His  
50 55 60

ccacgattgc aatgacagcc 210

<210> 56

<211> 60

<212> PRT

<213> Conus arenatus

&lt;400&gt; 56

Met Gly Lys Leu Thr Ile Leu Val Leu Val Ala Ala Val Leu Leu Ser  
 1 5 10 15

Thr Gln Ala Met Val Gln Asp Gln Pro Ala Gly Arg Asp Ala Val Pro  
 20 25 30

Arg Asp Asp Asn Pro Gly Gly Thr Ser Gly Lys Phe Val Asn Ala Gln  
 35 40 45

Arg Gln Tyr Gly Cys Pro Pro Gly Leu Trp Cys His  
 50 55 60

&lt;210&gt; 57

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Conus arenatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(11)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 5 and 6 is  
 Pro or hydroxy-Pro; Xaa at residue 9 is Trp (D or L) or bromo-Trp  
 (D or L); Xaa at residue 2 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 57

Xaa Xaa Gly Cys Xaa Xaa Gly Leu Xaa Cys His  
 1 5 10

&lt;210&gt; 58

&lt;211&gt; 213

&lt;212&gt; DNA

&lt;213&gt; Conus aurisiacus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(189)

&lt;400&gt; 58

atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15

atc cct tca gat cgt gca tct gat ggc agg aat gcc gca gtc aac gag 96  
 Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu  
 20 25 30

aga gcg cct tgg ctg gtc cct tcg aca atc acg act tgc tgt gga tat 144  
 Arg Ala Pro Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr  
 35 40 45

aat ccg ggg aca atg tgc cct cct tgc agg tgc gat aat acc tgt 189  
 Asn Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asp Asn Thr Cys  
 50 55 60

taaccaaaaa aaaaaaaaaa aaaa 213

&lt;210&gt; 59

&lt;211&gt; 63

<212> PRT  
 <213> Conus aurisiacus

<400> 59  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu  
 20 25 30  
 Arg Ala Pro Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr  
 35 40 45  
 Asn Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asp Asn Thr Cys  
 50 55 60

<210> 60  
 <211> 30  
 <212> PRT  
 <213> Conus aurisiacus

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa at residues 2, 6, 17, 22 and 23 is Pro or hydroxy-Pro; Xaa at  
 residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue  
 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 60  
 Ala Xaa Xaa Leu Val Xaa Ser Thr Ile Thr Thr Cys Cys Gly Xaa Asn  
 1 5 10 15  
 Xaa Gly Thr Met Cys Xaa Xaa Cys Arg Cys Asp Asn Thr Cys  
 20 25 30

<210> 61  
 <211> 202  
 <212> DNA  
 <213> Conus bandanus

<220>  
 <221> CDS  
 <222> (1)..(183)

<400> 61  
 atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
 gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96  
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu  
 20 25 30  
 tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144  
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp  
 35 40 45  
 aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193  
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys

50 55 60

gaaggatcc 202

<210> 62  
 <211> 61  
 <212> PRT  
 <213> Conus bandanus

<400> 62  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu  
 20 25 30  
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp  
 35 40 45  
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys  
 50 55 60

<210> 63  
 <211> 11  
 <212> PRT  
 <213> Conus bandanus

<220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-  
 Tyr

<400> 63  
 Ala Cys Cys Gly Xaa Lys Leu Cys Ser Xaa Cys  
 1 5 10

<210> 64  
 <211> 359  
 <212> DNA  
 <213> Conus characteristicus

<220>  
 <221> CDS  
 <222> (7)..(246)

<400> 64  
 ggatcc atg aaa ctg acg tgc gtg gtg atc atc gcc gcg ctg ttc ctg 48  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Ala Leu Phe Leu  
 1 5 10  
 acg gcc tgt cag ctg aat aca gct gat gac tcc aga gat aag cag gag 96  
 Thr Ala Cys Gln Leu Asn Thr Ala Asp Asp Ser Arg Asp Lys Gln Glu  
 15 20 25 30  
 tac cgt gca gtg agg ttg aga gac gga atg cgg aat ttc aaa ggt tcc 144  
 Tyr Arg Ala Val Arg Leu Arg Asp Gly Met Arg Asn Phe Lys Gly Ser  
 35 40 45

aag cgc aac tgc ggg gaa caa ggt gaa ggt tgt gct act cgc cca tgc 192  
 Lys Arg Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys  
                   50                                  55                                  60

tgc tct ggt ctg agt tgc gtt ggc agc cgt cca gga ggc ctg tgc cag 240  
 Cys Ser Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln  
                   65                                  70                                  75

tac ggc taatagtctg gcatctgata tttccctctt gcaactctacc ttcttttgcc 296  
 Tyr Gly  
           80

tgatgcatgt ttacttgtgt gtggatcatga accactcagt agctacacct ccgaaggacg 356

tgc 359

<210> 65

<211> 80

<212> PRT

<213> Conus characteristicus

<400> 65

Met Lys Leu Thr Cys Val Val Ile Ile Ala Ala Leu Phe Leu Thr Ala  
 1                  5                                  10                                  15

Cys Gln Leu Asn Thr Ala Asp Asp Ser Arg Asp Lys Gln Glu Tyr Arg  
                   20                                  25                                  30

Ala Val Arg Leu Arg Asp Gly Met Arg Asn Phe Lys Gly Ser Lys Arg  
                   35                                  40                                  45

Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys Cys Ser  
                   50                                  55                                  60

Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln Tyr Gly  
 65                                  70                                  75                                  80

<210> 66

<211> 31

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa at residues 4 and 7 is Glu or gamma-carboxy-Glu; Xaa at  
 residues 13 and 25 is Pro or hydroxy-Pro; Xaa at residue 31 is Tyr,  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 66

Asn Cys Gly Xaa Gln Gly Xaa Gly Cys Ala Thr Arg Xaa Cys Cys Ser  
 1                  5                                  10                                  15

Gly Leu Ser Cys Val Gly Ser Arg Xaa Gly Gly Leu Cys Gln Xaa  
                   20                                  25                                  30

<210> 67

<211> 349

<212> DNA

<213> Conus characteristicus

<220>

<221> CDS

<222> (1)..(270)

<400> 67

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc	48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile	
1 5 10 15	

ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac	96
Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His	
20 25 30	

ctg aag aga ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc	144
Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys	
35 40 45	

tct ggc act tgc cat cgt cgt gag gac ggc aag tgt cgg ggt act tgc	192
Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys	
50 55 60	

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt	240
Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe	
65 70 75 80	

tac cga gga tgc acg tgt tcg tgt caa ggt tgattaattg actcttttaa	290
Tyr Arg Gly Cys Thr Cys Ser Cys Gln Gly	
85 90	

ctcgttgaac gattgaaaaa aaaaatttta gagcaatatg ttcgagaaaa accgaagac	349
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<210> 68

<211> 90

<212> PRT

<213> Conus characteristicus

<400> 68

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1 5 10 15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
20 25 30

Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
35 40 45

Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys
50 55 60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
65 70 75 80

Tyr Arg Gly Cys Thr Cys Ser Cys Gln Gly
85 90

<210> 69

<211> 43

<212> PRT



<213> Conus characteristic

<220>

<221> PEPTIDE

<222> (1)..(43)

<223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 69

Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly  
1 5 10 15

Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His  
20 25 30

His Phe Xaa Arg Gly Cys Thr Cys Ser Cys Gln  
35 40

<210> 70

<211> 346

<212> DNA

<213> Conus characteristic

<220>

<221> CDS

<222> (1)..(264)

<400> 70

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48  
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile  
1 5 10 15

ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96  
Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
20 25 30

cgg aag agc ggc ttc tac ggt act ctg gca atg tct gcc aga gga tgc 144  
Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys  
35 40 45

tct ggc act tgc cat cgt cgt gag gac ggc aag tgt cgg ggt act tgc 192  
Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys  
50 55 60

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240  
Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe  
65 70 75 80

tac cga gga tgc acg tgt aca tgt taagggtgat taattgactc ttttaactcg 294  
Tyr Arg Gly Cys Thr Cys  
85

ttgaaccgat taaaaaaaaa attagacgaa tatgttcgag aaaaccgaag ac 346

<210> 71

<211> 88

<212> PRT

<213> Conus characteristic

&lt;400&gt; 71

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile  
 1 5 10 15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
 20 25 30

Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys  
 35 40 45

Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys  
 50 55 60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe  
 65 70 75 80

Tyr Arg Gly Cys Thr Cys Thr Cys  
 85

&lt;210&gt; 72

&lt;211&gt; 42

&lt;212&gt; PRT

&lt;213&gt; Conus characteristicus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(42)

<223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues  
 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 72

Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly  
 1 5 10 15

Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His  
 20 25 30

His Phe Xaa Arg Gly Cys Thr Cys Thr Cys  
 35 40

&lt;210&gt; 73

&lt;211&gt; 348

&lt;212&gt; DNA

&lt;213&gt; Conus characteristicus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(264)

&lt;400&gt; 73

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile  
 1 5 10 15

ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96  
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
 20 25 30

cgg aag agc ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc 144

Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys  
           35                                  40                                  45

tct ggc act tgc cgt cgt cat cgg gac ggc aag tgt cgg ggt act tgc           192  
 Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys  
           50                                  55                                  60

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt           240  
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe  
           65                                  70                                  75                                  80

tac cga gga tgc acg tgt aca tgt taagggtgat taattcgatc ttttaactcg           294  
 Tyr Arg Gly Cys Thr Cys Thr Cys  
                                   85

ttgaacgatt aaaaaaaaaa ttttagacga atatgttcga gaaaaaccga agac           348

<210> 74  
 <211> 88  
 <212> PRT  
 <213> Conus characteristicus

<400> 74  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile  
 1                                  5                                  10                                  15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
                                   20                                  25                                  30

Arg Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys  
           35                                  40                                  45

Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys  
           50                                  55                                  60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe  
           65                                  70                                  75                                  80

Tyr Arg Gly Cys Thr Cys Thr Cys  
                                   85

<210> 75  
 <211> 42  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(42)  
 <223> Xaa at residues 23, 25 and 35 is Tyr, <sup>125</sup>I-Tyr, mono-iodo-Tyr,  
           di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 75  
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly  
 1                                  5                                  10                                  15

Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His  
                                   20                                  25                                  30

His Phe Xaa Arg Gly Cys Thr Cys Thr Cys

```

35                                40

<210> 76
<211> 349
<212> DNA
<213> Conus characteristicus

<220>
<221> CDS
<222> (1)..(264)

<400> 76
atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc      48
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1          5          10          15

ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac      96
Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
          20          25          30

ctg aag aga ggc ttc tac ggt act ctg gca atg tct acc aga gga tgc      144
Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
          35          40          45

tct ggc act tgc cgt cgt cat cgg gac ggc aag tgt cgg ggt act tgc      192
Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
          50          55          60

gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt      240
Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
65          70          75          80

tac cga gga tgc acg tgt aca tgt taagggtgat taattgactc ttttaactcg      294
Tyr Arg Gly Cys Thr Cys Thr Cys
          85

ttgaacgatt aaaaaaaaaa atttttagagc aatatgttcg agaaaaaccg aagac      349

<210> 77
<211> 88
<212> PRT
<213> Conus characteristicus

<400> 77
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1          5          10          15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
          20          25          30

Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Thr Arg Gly Cys
          35          40          45

Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly Thr Cys
          50          55          60

Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe
65          70          75          80

Tyr Arg Gly Cys Thr Cys Thr Cys

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85

<210> 78  
 <211> 42  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(42)  
 <223> Xaa at residues 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 78  
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys  
 35 40

<210> 79  
 <211> 345  
 <212> DNA  
 <213> Conus characteristicus

<220>  
 <221> CDS  
 <222> (1)..(264)

<400> 79  
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ttt ctt ttc acc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Phe Leu Phe Thr  
 1 5 10 15  
 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96  
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
 20 25 30  
 ctg aag aga ggc ttc tac ggt act ctg gca atg tct tcc aga gga tgc 144  
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Ser Arg Gly Cys  
 35 40 45  
 tct ggc act tgc cat cgt cgt gag gac ggc aag tgt cgg ggt act tgc 192  
 Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys  
 50 55 60  
 gac tgc tcc gga tac agc tat tgt cgc tgc ggt gac gct cac cat ttt 240  
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe  
 65 70 75 80  
 tac cga gga tgt acg tgt aca tgt taagggtgat taattgactc ttttaactcg 294  
 Tyr Arg Gly Cys Thr Cys Thr Cys  
 85  
 ttgaacgatt aaaaaaaaaat ttagagcaat atgttcgaga aaaccgaaga c 345

<210> 80

<211> 88  
 <212> PRT  
 <213> Conus characteristicus

<400> 80  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Phe Leu Phe Thr  
 1 5 10 15  
 Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
 20 25 30  
 Leu Lys Arg Gly Phe Tyr Gly Thr Leu Ala Met Ser Ser Arg Gly Cys  
 35 40 45  
 Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly Thr Cys  
 50 55 60  
 Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His His Phe  
 65 70 75 80  
 Tyr Arg Gly Cys Thr Cys Thr Cys  
 85

<210> 81  
 <211> 42  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(42)  
 <223> Xaa at residue 10 is Glu or gamma-carboxy-Glu; Xaa at residues  
 23, 25 and 35 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr

<400> 81  
 Gly Cys Ser Gly Thr Cys His Arg Arg Xaa Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Xaa Ser Xaa Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Xaa Arg Gly Cys Thr Cys Thr Cys  
 35 40

<210> 82  
 <211> 344  
 <212> DNA  
 <213> Conus characteristicus

<220>  
 <221> CDS  
 <222> (1)..(264)

<400> 82  
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc atc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile  
 1 5 10 15  
 ctg cca tcc agc cag cag gaa gga gat gtc cag gca aga aaa acg cac 96

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Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
      20                      25                      30

ctg aag agc ggc ttc tac ggt act ctg gca atg tct gcc aga gga tgc      144
Leu Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys
      35                      40                      45

tct ggc act tgc cat cgt cgt caa aac ggc gag tgt cag ggt act tgc      192
Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly Thr Cys
      50                      55                      60

gac tgc gac gga cac gac cat tgt gac tgc ggt gac act ctc ggt act      240
Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu Gly Thr
      65                      70                      75                      80

tac tca gga tgc gtg tgt ata tgt taagggtgat taattgactc ttttaactcg      294
Tyr Ser Gly Cys Val Cys Ile Cys
      85

ttgaacgatt aaaaaaattt agagcaatat gttcgagaaa aaccgaagac      344

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<210> 83
<211> 88
<212> PRT
<213> Conus characteristicus

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<400> 83
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Ile
1                      5                      10                      15

Leu Pro Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His
      20                      25                      30

Leu Lys Ser Gly Phe Tyr Gly Thr Leu Ala Met Ser Ala Arg Gly Cys
      35                      40                      45

Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly Thr Cys
      50                      55                      60

Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu Gly Thr
      65                      70                      75                      80

Tyr Ser Gly Cys Val Cys Ile Cys
      85

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<210> 84
<211> 42
<212> PRT
<213> Conus characteristicus

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<220>
<221> PEPTIDE
<222> (1)..(42)
<223> Xaa at residue 13 is Glu or gamma-carboxy-Glu; Xaa at residue 35
      is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr

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<400> 84
Gly Cys Ser Gly Thr Cys His Arg Arg Gln Asn Gly Xaa Cys Gln Gly
1                      5                      10                      15

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Thr Cys Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu  
                   20                                  25                                  30

Gly Thr Xaa Ser Gly Cys Val Cys Ile Cys  
                   35                                  40

<210> 85  
 <211> 422  
 <212> DNA  
 <213> Conus characteristicus

<220>  
 <221> CDS  
 <222> (7)..(258)

<400> 85  
 gttaca atg cat ctg tca ctg gca cgc tca gct gtc ttg atg ttg ctt 48  
           Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu  
           1                                  5                                  10

ctg ctg ttt gcc ttg gac aac ttc gtt ggg gtc cag cca gga cag ata 96  
 Leu Leu Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile  
 15                                  20                                  25                                  30

aca aga gat gtg gac aac cgc cgt aac cgg caa tcg cga tgg aag cca 144  
 Thr Arg Asp Val Asp Asn Arg Arg Asn Arg Gln Ser Arg Trp Lys Pro  
                                   35                                  40                                  45

agg agt ctc ttc aag tca ctt cat aaa cga gca tcg tgt gga ggg act 192  
 Arg Ser Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr  
                                   50                                  55                                  60

tgc acg gaa agt gcc gat tgc cct tcc acg tgt agt act tgc tta cat 240  
 Cys Thr Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His  
                                   65                                  70                                  75

gct caa tgc gag tca aca tgatgtcgca ctacagctct tctctacagt 288  
 Ala Gln Cys Glu Ser Thr  
                   80

gtgtacatcg accgtacgac gcatctttta tttctttggc tgtttcattc gttttcttgt 348

gttcataaca tgcggagccc ttccggttacc tctactgctc tacacttaac ctgataacca 408

gaaaatccag tact 422

<210> 86  
 <211> 84  
 <212> PRT  
 <213> Conus characteristicus

<400> 86  
 Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu Leu  
 1                                  5                                  10                                  15

Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile Thr Arg  
                   20                                  25                                  30

Asp Val Asp Asn Arg Arg Asn Arg Gln Ser Arg Trp Lys Pro Arg Ser



35                      40                      45  
 Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr Cys Thr  
     50                      55                      60  
 Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His Ala Gln  
     65                      70                      75                      80  
 Cys Glu Ser Thr

<210> 87  
 <211> 28  
 <212> PRT  
 <213> Conus characteristicus  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residues 9 and 26 is Glu or gamma-carboxy-Glu; Xaa at  
       residue 14 is Pro or hydroxy-Pro

<400> 87  
 Ala Ser Cys Gly Gly Thr Cys Thr Xaa Ser Ala Asp Cys Xaa Ser Thr  
     1                      5                      10                      15  
 Cys Ser Thr Cys Leu His Ala Gln Cys Xaa Ser Thr  
                     20                      25

<210> 88  
 <211> 426  
 <212> DNA  
 <213> Conus characteristicus

<220>  
 <221> CDS  
 <222> (7)..(258)

<400> 88  
 gttaca atg cat ctg tca ctg gca cgc tca gct gtt ttg atg ttg ctt                      48  
       Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu  
       1                      5                      10

ctg ctg ttt gcc ttg gac aac ttc gtt ggg gtc caa cca gga cag ata                      96  
 Leu Leu Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile  
     15                      20                      25                      30

act aga gat gtg gac aac cgc cgt aac ctg caa tcg cga tgg aag cca                      144  
 Thr Arg Asp Val Asp Asn Arg Arg Asn Leu Gln Ser Arg Trp Lys Pro  
                     35                      40                      45

agg agt ctc ttc aag tca ctt cat aaa cga gca tcg tgt gga ggg act                      192  
 Arg Ser Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr  
                     50                      55                      60

tgc acg gaa agt gcc gat tgc cct tcc acg tgt agt act tgc tta cat                      240  
 Cys Thr Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His  
                     65                      70                      75

gct caa tgc gag tga aca tgatgtcgca ctacagctct tctctacagt                      288

Ala Gln Cys Glu Thr  
80

gtgtacatcg accgaccgta cgacgcatct tttatttctt tgtctgtttc attcgttttc 348

ttgagttcat aacatgcgga gcccttcctg tacctctact gctctacact taagctgata 408

accagaaaat ccagtact 426

<210> 89

<211> 82

<212> PRT

<213> Conus characteristicus

<400> 89

Met His Leu Ser Leu Ala Arg Ser Ala Val Leu Met Leu Leu Leu Leu  
1 5 10 15

Phe Ala Leu Asp Asn Phe Val Gly Val Gln Pro Gly Gln Ile Thr Arg  
20 25 30

Asp Val Asp Asn Arg Arg Asn Leu Gln Ser Arg Trp Lys Pro Arg Ser  
35 40 45

Leu Phe Lys Ser Leu His Lys Arg Ala Ser Cys Gly Gly Thr Cys Thr  
50 55 60

Glu Ser Ala Asp Cys Pro Ser Thr Cys Ser Thr Cys Leu His Ala Gln  
65 70 75 80

Cys Glu

<210> 90

<211> 25

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> Xaa at residues 8 and 25 is Glu or gamma-carboxy-Glu; Xaa at  
residue 13 is Pro or hydroxy-Pro

<400> 90

Ser Cys Gly Gly Thr Cys Thr Xaa Ser Ala Asp Cys Xaa Ser Thr Cys  
1 5 10 15

Ser Thr Cys Leu His Ala Gln Cys Xaa  
20 25

<210> 91

<211> 220

<212> DNA

<213> Conus circumcissus

<220>

<221> CDS

<222> (28)..(189)

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<400> 91
tgtgtgtgtg tggttctg tccagca ttt gat ggc agg aat gcc gca gtc aac 54
Phe Asp Gly Arg Asn Ala Ala Val Asn
1 5

gag aga gcg cct tgg acg gtc gtt ttg tcc acc acg aat tgc tgc ggt 102
Glu Arg Ala Pro Trp Thr Val Val Leu Ser Thr Thr Asn Cys Cys Gly
10 15 20 25

tat aat acg atg gaa ttc tgc cct gct tgc atg tgc act tat tcc tgt 150
Tyr Asn Thr Met Glu Phe Cys Pro Ala Cys Met Cys Thr Tyr Ser Cys
30 35 40

cca aaa aag aaa aaa cca gga aaa ggc cgc aga aac aac tgatgctcca 199
Pro Lys Lys Lys Lys Pro Gly Lys Gly Arg Arg Asn Asn
45 50

ggaccctctg aaccacgacg t 220

<210> 92
<211> 54
<212> PRT
<213> Conus circumcissus

<400> 92
Phe Asp Gly Arg Asn Ala Ala Val Asn Glu Arg Ala Pro Trp Thr Val
1 5 10 15

Val Leu Ser Thr Thr Asn Cys Cys Gly Tyr Asn Thr Met Glu Phe Cys
20 25 30

Pro Ala Cys Met Cys Thr Tyr Ser Cys Pro Lys Lys Lys Lys Pro Gly
35 40 45

Lys Gly Arg Arg Asn Asn
50

<210> 93
<211> 43
<212> PRT
<213> Conus circumcissus

<220>
<221> PEPTIDE
<222> (1)..(43)
<223> Xaa at residue 19 is Glu or gamma-carboxy-Glu; Xaa at residues 2,
22, 31 and 36 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D
or L) or bromo-Trp (D or L); Xaa at residues 15 and 28 is Tyr, 125
I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 93
Ala Xaa Xaa Thr Val Val Leu Ser Thr Thr Asn Cys Cys Gly Xaa Asn
1 5 10 15

Thr Met Xaa Phe Cys Xaa Ala Cys Met Cys Thr Xaa Ser Cys Xaa Lys
20 25 30

Lys Lys Lys Xaa Gly Lys Gly Arg Arg Asn Asn
35 40

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<210> 94  
 <211> 64  
 <212> PRT  
 <213> Conus consors

<400> 94  
 Gly Ile Phe Val Gly Val Gln Pro Glu Gln Ile Thr Arg Asp Val Asp  
 1 5 10 15  
 Lys Gly Tyr Ser Thr Asp Asp Gly His Asp Leu Leu Ser Leu Leu Lys  
 20 25 30  
 Gln Ile Ser Leu Arg Ala Cys Thr Gly Ser Cys Asn Ser Asp Ser Glu  
 35 40 45  
 Cys Tyr Asn Phe Cys Asp Cys Ile Gly Thr Arg Cys Glu Ala Gln Lys  
 50 55 60

<210> 95  
 <211> 27  
 <212> PRT  
 <213> Conus consors

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 11 and 24 is Glu or gamma-carboxy-Glu; Xaa at  
 residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr

<400> 95  
 Ala Cys Thr Gly Ser Cys Asn Ser Asp Ser Xaa Cys Xaa Asn Phe Cys  
 1 5 10 15  
 Asp Cys Ile Gly Thr Arg Cys Xaa Ala Gln Lys  
 20 25

<210> 96  
 <211> 27  
 <212> PRT  
 <213> Conus delesstii

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 13 and 16 is Glu or gamma-carboxy-Glu; Xaa at  
 residue 4 is Pro or hydroxy-Pro; Xaa at residue 25 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 96  
 Ala Cys Lys Xaa Lys Asn Asn Leu Cys Ala Ile Thr Xaa Met Ala Xaa  
 1 5 10 15  
 Cys Cys Ser Gly Phe Cys Leu Ile Xaa Arg Cys  
 20 25

<210> 97  
 <211> 375  
 <212> DNA

<213> Conus distans

<220>

<221> CDS

<222> (24)..(260)

<400> 97

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53  
Met Ser Gly Leu Gly Ile Met Val Leu Thr  
1 5 10

ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101  
Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu  
15 20 25

aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149  
Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser  
30 35 40

atc act cgg aga aat gta gat cag gag tgc att gac gcc tgt cag ctg 197  
Ile Thr Arg Arg Asn Val Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu  
45 50 55

gag gac aag aat tgc tgt ggc aga aca gat gga gaa ccc aga tgt gcg 245  
Glu Asp Lys Asn Cys Cys Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala  
60 65 70

aaa atc tgc ctc gga taatttctgt acgctgtctc attcattatt tcatccgtac 300  
Lys Ile Cys Leu Gly  
75

gagtgtaaac gagacctatt agaaagtcga aggttggtgcg taatttgata agcattgttt 360

gctgggacga acgga 375

<210> 98

<211> 79

<212> PRT

<213> Conus distans

<400> 98

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro  
1 5 10 15

Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg  
20 25 30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Arg Asn Val  
35 40 45

Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu Glu Asp Lys Asn Cys Cys  
50 55 60

Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala Lys Ile Cys Leu Gly  
65 70 75

<210> 99

<211> 32

<212> PRT

<213> Conus distans

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<220>
<221> PEPTIDE
<222> (1)..(32)
<223> Xaa at residues 5, 13 and 24 is Glu or gamma-carboxy-Glu; Xaa at
      residue 25 is Pro or hydroxy-Pro

<400> 99
Asn Val Asp Gln Xaa Cys Ile Asp Ala Cys Gln Leu Xaa Asp Lys Asn
1          5          10          15

Cys Cys Gly Arg Thr Asp Gly Xaa Xaa Arg Cys Ala Lys Ile Cys Leu
      20          25          30

<210> 100
<211> 376
<212> DNA
<213> Conus distans

<220>
<221> CDS
<222> (24)..(260)

<400> 100
gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc      53
              Met Ser Gly Leu Gly Ile Met Val Leu Thr
              1          5

ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag      101
Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu
              15          20          25

aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca      149
Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser
              30          35          40

atc act cgg aca gaa aca gat cag gag tgc att gac atc tgt aag cag      197
Ile Thr Arg Thr Glu Thr Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln
              45          50          55

gag gac aag aaa tgc tgc ggc aga tca aat gga gaa ccc aca tgt gcg      245
Glu Asp Lys Lys Cys Cys Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala
              60          65          70

aaa atc tgc ctc gga taatttctgt acgctgtctc gttcattatt tcgtcagtac      300
Lys Ile Cys Leu Gly
75

gagttttaaac gagacctatt agaaagtcga aggttcgtgc ttaatttgat aagcattggt      360

tgctgggatg aacgga      376

<210> 101
<211> 79
<212> PRT
<213> Conus distans

<400> 101
Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro
1          5          10          15

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Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg  
                   20                  25                  30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Thr Glu Thr  
           35                  40                  45

Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln Glu Asp Lys Lys Cys Cys  
       50                  55                  60

Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala Lys Ile Cys Leu Gly  
       65                  70                  75

<210> 102

<211> 32

<212> PRT

<213> Conus distans

<220>

<221> PEPTIDE

<222> (1)..(32)

<223> Xaa at residues 1, 5, 13 and 24 is Glu or gamma-carboxy-Glu; Xaa  
       at residue 25 is Pro or hydroxy-Pro

<400> 102

Xaa Thr Asp Gln Xaa Cys Ile Asp Ile Cys Lys Gln Xaa Asp Lys Lys  
   1                  5                  10                  15

Cys Cys Gly Arg Ser Asn Gly Xaa Xaa Thr Cys Ala Lys Ile Cys Leu  
                   20                  25                  30

<210> 103

<211> 376

<212> DNA

<213> Conus distans

<220>

<221> CDS

<222> (24)..(260)

<400> 103

gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg cta acc 53  
                                   Met Ser Gly Leu Gly Ile Met Val Leu Thr  
                                   1                  5                  10

ctt cta ctt ctt gtg ccc atg gca acc agt caa cag gat gga gga gag 101  
   Leu Leu Leu Leu Val Pro Met Ala Thr Ser Gln Gln Asp Gly Gly Glu  
                   15                  20                  25

aag cag gcg atg caa agg gac gca atc aac gtc gca cca gga aca tca 149  
   Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Ala Pro Gly Thr Ser  
                   30                  35                  40

atc act cgg aga gaa aca gat cag gag tgc att gac acc tgt gag cag 197  
   Ile Thr Arg Arg Glu Thr Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln  
                   45                  50                  55

gag gac aag aaa tgc tgc ggc aga aca aat gga gaa ccc gta tgt gcg 245  
   Glu Asp Lys Lys Cys Cys Gly Arg Thr Asn Gly Glu Pro Val Cys Ala  
           60                  65                  70

aaa atc tgc ttc gga taatttctgt acgctgtctc attcataatt tcatcagtac 300  
 Lys Ile Cys Phe Gly  
 75

gagtttaaac gagacctatt agaaagtcga aggttcgtgc ttaatttgat aagcattggt 360

tgctgggatg aacgga 376

<210> 104  
 <211> 79  
 <212> PRT  
 <213> Conus distans

<400> 104  
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Pro  
 1 5 10 15

Met Ala Thr Ser Gln Gln Asp Gly Gly Glu Lys Gln Ala Met Gln Arg  
 20 25 30

Asp Ala Ile Asn Val Ala Pro Gly Thr Ser Ile Thr Arg Arg Glu Thr  
 35 40 45

Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln Glu Asp Lys Lys Cys Cys  
 50 55 60

Gly Arg Thr Asn Gly Glu Pro Val Cys Ala Lys Ile Cys Phe Gly  
 65 70 75

<210> 105  
 <211> 32  
 <212> PRT  
 <213> Conus distans

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residues 1, 5, 11, 13 and 24 is Glu or gamma-carboxy-Glu;  
 Xaa at residue 25 is Pro or hydroxy-Pro

<400> 105  
 Xaa Thr Asp Gln Xaa Cys Ile Asp Thr Cys Xaa Gln Xaa Asp Lys Lys  
 1 5 10 15

Cys Cys Gly Arg Thr Asn Gly Xaa Xaa Val Cys Ala Lys Ile Cys Phe  
 20 25 30

<210> 106  
 <211> 250  
 <212> DNA  
 <213> Conus ermineus

<220>  
 <221> CDS  
 <222> (1)..(219)

<400> 106  
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15



ttc act tca gat cgt gca tcg gat gac agg aat acc aac gac aaa gca 96  
Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala  
20 25 30

tct	cgc	ctg	ctc	tct	cac	gtt	gtc	agg	gga	tgc	tgt	ggc	aag	tat	ccc	144
Ser	Arg	Leu	Leu	Ser	His	Val	Val	Arg	Gly	Cys	Cys	Gly	Lys	Tyr	Pro	
		35					40					45				

aat gct gcc tgt cat cct tgc ggt tgt aca gtg ggt agg cca ccg tat 192  
Asn Ala Ala Cys His Pro Cys Gly Cys Thr Val Gly Arg Pro Pro Tyr  
50 55 60

tgt gac aga ccc agt ggt gga gga cgc tgatgctcca ggacctctg 239  
Cys Asp Arg Pro Ser Gly Gly Gly Arg  
65 70

aaccacgacg t 250

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<210> 107
<211> 73
<212> PRT
<213> Conus ermineus
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<400> 107
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1          5          10          15
```

Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala  
20 25 30

Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Lys Tyr Pro  
35 40 45

Asn Ala Ala Cys His Pro Cys Gly Cys Thr Val Gly Arg Pro Pro Tyr  
50 55 60

Cys Asp Arg Pro Ser Gly Gly Gly Arg  
65 70

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<210> 108
<211> 30
<212> PRT
<213> Conus ermineus
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<220>
<221> PEPTIDE
<222> (1)..(30)
<223> Xaa at residue7, 13, 21, 22 and 27 is Pro or hydroxy-Pro; Xaa at
residues 6 and 23 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
O-sulpho-Tyr or O-phospho-Tyr

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<400> 108  
Gly Cys Cys Gly Lys Xaa Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys  
1 5 10 15

Thr Val Gly Arg Xaa Xaa Xaa Cys Asp Arg Xaa Ser Gly Gly  
20 25 30

<210> 109

<211> 241  
 <212> DNA  
 <213> *Conus generalis*

<220>  
 <221> CDS  
 <222> (1)..(210)

<400> 109  
 gga tcc atg atg tct aaa ctg gga gtc ttg ttg acc atc tgt ctg gtt 48  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val  
 1 5 10 15  
 ctg ttt ccc ctt act gct ctt cca ctg gat gga gaa caa cct gta gac 96  
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp  
 20 25 30  
 cga cat gcc gag cat atg cag gat gac aat tca gct gca cag aac ccc 144  
 Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro  
 35 40 45  
 tgg gtt att gcc atc aga cag tgt tgc acg ttc tgc aac ttt gga tgc 192  
 Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys  
 50 55 60  
 cag cct tgt tgc gtc ccc tgataacgtg ttgatgacca actttctcga g 241  
 Gln Pro Cys Cys Val Pro  
 65 70

<210> 110  
 <211> 70  
 <212> PRT  
 <213> *Conus generalis*

<400> 110  
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val  
 1 5 10 15  
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp  
 20 25 30  
 Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro  
 35 40 45  
 Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys  
 50 55 60  
 Gln Pro Cys Cys Val Pro  
 65 70

<210> 111  
 <211> 16  
 <212> PRT  
 <213> *Conus generalis*

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 12 and 16 is  
 Pro or hydroxy-Pro

<400> 111  
 Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa  
 1 5 10 15

<210> 112  
 <211> 404  
 <212> DNA  
 <213> Conus geographus

<220>  
 <221> CDS  
 <222> (18)..(242)

<400> 112  
 gcaagatcat cagcaga atg aac ctg acg tgc gtg ttg atc atc gcc gtg 50  
 Met Asn Leu Thr Cys Val Leu Ile Ile Ala Val  
 1 5 10  
 ctg ttt ctg acg gcc tgc cag ctc att gca gct gat gac tcc aga gat 98  
 Leu Phe Leu Thr Ala Cys Gln Leu Ile Ala Ala Asp Asp Ser Arg Asp  
 15 20 25  
 aac cag aag cac cgt gca gtg agg atg aga gac gca ttg aag aat ttc 146  
 Asn Gln Lys His Arg Ala Val Arg Met Arg Asp Ala Leu Lys Asn Phe  
 30 35 40  
 aaa gat tcc agg gcg tgc tcc ggt aga ggt tct aga tgt cct ccc caa 194  
 Lys Asp Ser Arg Ala Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln  
 45 50 55  
 tgc tgc atg ggt ttg acg tgc ggt cgt gag tat cca ccc aga tgc ggt 242  
 Cys Cys Met Gly Leu Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys Gly  
 60 65 70 75  
 tgatatacgg tgaacaactg atattttcccc tctgtgctct accctctttt gcctgattca 302  
 cccacaccta tgtgtgggtca tgaaccactc agtacctaca cctctgggtg cttcagagga 362  
 cgtatatatta aataaaacca cattgcaatg aaaaaaaaaa aa 404

<210> 113  
 <211> 75  
 <212> PRT  
 <213> Conus geographus

<400> 113  
 Met Asn Leu Thr Cys Val Leu Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Cys Gln Leu Ile Ala Ala Asp Asp Ser Arg Asp Asn Gln Lys His Arg  
 20 25 30  
 Ala Val Arg Met Arg Asp Ala Leu Lys Asn Phe Lys Asp Ser Arg Ala  
 35 40 45

Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln Cys Cys Met Gly Leu  
 50 55 60

Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys Gly  
 65 70 75

<210> 114  
 <211> 27  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 22 is Glu or gamma-carboxy-Glu; Xaa at residues  
 10, 11, 24 and 25 is Pro or hydroxy-Pro; Xaa at residue 23 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 114  
 Ala Cys Ser Gly Arg Gly Ser Arg Cys Xaa Xaa Gln Cys Cys Met Gly  
 1 5 10 15

Leu Thr Cys Gly Arg Xaa Xaa Xaa Xaa Arg Cys  
 20 25

<210> 115  
 <211> 9  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(9)  
 <223> Xaa at residue 7 is Pro or hydroxy-Pro

<400> 115  
 Cys Phe Ile Arg Asn Cys Xaa Lys Gly  
 1 5

<210> 116  
 <211> 360  
 <212> DNA  
 <213> Conus geographus

<220>  
 <221> CDS  
 <222> (1)..(213)

<400> 116  
 tgc tgc ccg agt agc aaa gag gat tcc ctg aac tgc att gag acc atg 48  
 Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met  
 1 5 10 15

gcg acc acg gcc acg tgc atg aag tcc aac aag ggg gag atc tac tcc 96  
 Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser  
 20 25 30

tat gcg tgc ggc tac tgc ggc aag aag aag gag agc tgt ttc ggc gac 144

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp  
           35                          40                          45

aaa aag cca gtg act gac tac cag tgc cag acg cgg aac att ccc aac           192  
 Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn  
       50                          55                          60

ccc tgc ggc ggc gct gct ctc tgaaggcacc aacagcacca acagcacgat           243  
 Pro Cys Gly Gly Ala Ala Leu  
       65                          70

ctctgtgttt tcgtcactgc atttatgacg tcaaaaccac gtcatgcatg atgacgacga   303

tctcggctat ggcatgtatt gaagaatgga aataaaccta gttttcagct gaaaaaa       360

<210> 117  
 <211> 71  
 <212> PRT  
 <213> Conus geographus

<400> 117  
 Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met  
   1                  5                          10                          15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser  
           20                          25                          30

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp  
           35                          40                          45

Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn  
       50                          55                          60

Pro Cys Gly Gly Ala Ala Leu  
       65                          70

<210> 118  
 <211> 71  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(71)  
 <223> Xaa at residues 7, 14, 29 and 43 is Glu or gamma-carboxy-Glu;  
       Xaa at residues 3, 51, 63 and 65 is Pro or hydroxy-Pro; Xaa at  
       residues 31, 33, 37 and 55 is Tyr, 125I-Tyr, mono-iodo-Tyr,  
       di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 118  
 Cys Cys Xaa Ser Ser Lys Xaa Asp Ser Leu Asn Cys Ile Xaa Thr Met  
   1                  5                          10                          15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Xaa Ile Xaa Ser  
           20                          25                          30

Xaa Ala Cys Gly Xaa Cys Gly Lys Lys Lys Xaa Ser Cys Phe Gly Asp  
           35                          40                          45

Lys Lys Xaa Val Thr Asp Xaa Gln Cys Gln Thr Arg Asn Ile Xaa Asn

50 55 60

Xaa Cys Gly Gly Ala Ala Leu  
65 70

<210> 119  
<211> 769  
<212> DNA  
<213> *Conus geographus*

<220>

<221> misc\_feature  
<222> (1)..(769)  
<223> n is unknown

<400> 119  
cgggcgctgc attccggacg tgaaacagca tcgccagcaa gtgggcatag tgcaagacac 60  
tcagaacaat gacgcacata gtctganaaa ataaccatgg gtatgcggat gangtttagt 120  
gtgtttcngc aggttgtcnt gggnaccact gtcgtttcct tcacntcacg tcgtggtcca 180  
aaatctcgtc gcggggaacc tattccgacc actgtaatca actacgggga gtgctgtaag 240  
gatccatcct gttgggttaa ggtgaaggat ttccagtgtc ctggagcaag tcctcccaac 300  
tgaaccacga catgtcgccc tctgcctgac ctgcttcacg ttccgtctct ttctgccact 360  
agaactcaac aactcgatcc aacagactcc tactttacct ccgtattctg aaactacttg 420  
gatttgattg tctttaatat ctactcacac ttgctgttat tacatcatcc aaaatttaac 480  
aagaacatga aaggtgtctg ttcaaacaaa atcaggcaat gacaangggg gaaagtctcc 540  
antctatctg aaaactgtca cctgtcactc tcttaaccag gtttanaact gantaccact 600  
anagctgttg tnccacatca ngatcagncc aatttgtann gtttcctttg caaaactttt 660  
gcctgaaatt cttgaaaaga aacgctcaca atgttgggaa gtgcttttna ttanctgaca 720  
anntgncanc atgttcnntt tcantaantc tnaaatgnaa acctctgtt 769

<210> 120  
<211> 68  
<212> PRT  
<213> *Conus geographus*

<400> 120  
Met Gly Met Arg Met Met Phe Ser Val Phe Leu Gln Val Val Leu Gly  
1 5 10 15  
Thr Thr Val Val Ser Phe Thr Ser Arg Arg Gly Pro Lys Ser Arg Arg  
20 25 30  
Gly Glu Pro Ile Pro Thr Thr Val Ile Asn Tyr Gly Glu Cys Cys Lys  
35 40 45  
Asp Pro Ser Cys Trp Val Lys Val Lys Asp Phe Gln Cys Pro Gly Ala

50 55 60

Ser Pro Pro Asn  
65

<210> 121  
<211> 36  
<212> PRT  
<213> Conus geographus

<220>  
<221> PEPTIDE  
<222> (1)..(36)  
<223> Xaa at residues 2 and 13 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 5, 18, 30, 35 and 35 is Pro or hydroxy-Pro; Xaa at residue 21 is Trp (D or L) or bromo-Trp (D or L);

<220>  
<221> PEPTIDE  
<222> (1)..(36)  
<223> Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 121  
Gly Xaa Xaa Ile Xaa Thr Thr Val Ile Asn Xaa Gly Xaa Cys Cys Lys  
1 5 10 15  
Asp Xaa Ser Cys Xaa Val Lys Val Lys Asp Phe Gln Cys Xaa Gly Ala  
20 25 30

Ser Xaa Xaa Asn  
35

<210> 122  
<211> 519  
<212> DNA  
<213> Conus geographus

<220>  
<221> CDS  
<222> (113)..(391)

<400> 122  
agccttgata cagagctggt atctgctggt aatacttgaa agaacaagtg ctgtgagcct 60  
tcattctctct ctgacttttag tttgggtcct ggagaaaacc ttgacgggca gt atg aaa 118  
Met Lys  
1  
att tac ctg tgt ctt gct ttt gtt ctg ctc ctg gct tct acc ata gtt 166  
Ile Tyr Leu Cys Leu Ala Phe Val Leu Leu Leu Ala Ser Thr Ile Val  
5 10 15  
gat tca ggg ctt ctt gat aaa att gag act ata aga aac tgg aaa cgc 214  
Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp Lys Arg  
20 25 30  
gat gac agc tat tgt gat gga tgc cta tgc acc ata tta aaa aaa gag 262  
Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Glu  
35 40 45 50

act tgc aca tcg act atg agc tgc agg gga aca tgc cga aaa gag tgg 310  
 Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Glu Trp  
                   55                  60                  65

cca tgt tgg gaa gaa gac tgc tac tgt act gaa atc caa ggt gga gct 358  
 Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly Gly Ala  
                   70                  75                  80

tgc gtc aca ccc tca gaa tgc aaa cct gga gag tgttgaggat tggagtggcc 411  
 Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu  
                   85                  90

agttccagca catacagcac catggtgccc tggacaatcg tctattgaat tgaatatgcc 471

tgtggcagga atctgtccta caaaataaaa aaatcataag ttaaaaaa 519

<210> 123  
 <211> 93  
 <212> PRT  
 <213> Conus geographus

<400> 123  
 Met Lys Ile Tyr Leu Cys Leu Ala Phe Val Leu Leu Leu Ala Ser Thr  
 1                  5                  10                  15  
 Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp  
                   20                  25                  30  
 Lys Arg Asp Asp Ser Tyr Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys  
                   35                  40                  45  
 Lys Glu Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys  
                   50                  55                  60  
 Glu Trp Pro Cys Trp Glu Glu Asp Cys Tyr Cys Thr Glu Ile Gln Gly  
 65                  70                  75                  80  
 Gly Ala Cys Val Thr Pro Ser Glu Cys Lys Pro Gly Glu  
                   85                  90

<210> 124  
 <211> 60  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(60)  
 <223> Xaa at residues 16, 36, 37, 43, 56 and 59 is Glu or gamma-  
 carboxy-Glu; Xaa at residues 33, 52 and 57 is Pro or hydroxy-Pro;  
 Xaa at residues 32 and 35 is Trp (D or L) or bromo-Trp (D or L);

<220>  
 <221> PEPTIDE  
 <222> (1)..(60)  
 <223> Xaa at residues 4 and 40 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 124



Asp Asp Ser Xaa Cys Asp Gly Cys Leu Cys Thr Ile Leu Lys Lys Xaa  
1 5 10 15

Thr Cys Thr Ser Thr Met Ser Cys Arg Gly Thr Cys Arg Lys Xaa Xaa  
20 25 30

Xaa Cys Xaa Xaa Xaa Asp Cys Xaa Cys Thr Xaa Ile Gln Gly Gly Ala  
35 40 45

Cys Val Thr Xaa Ser Xaa Cys Lys Xaa Gly Xaa Cys  
50 55 60

<210> 125  
<211> 409  
<212> DNA  
<213> Conus geographus

<220>  
<221> CDS  
<222> (17)..(313)

<400> 125  
aacgttgacg ggcagt atg aac att tac ctg tgt ctt gct ttt ctt ctg ttc 52  
Met Asn Ile Tyr Leu Cys Leu Ala Phe Leu Leu Phe  
1 5 10

ctg cct tct acc ata gtt gat tca ggg ctt ctt gat aaa att gag aca 100  
Leu Pro Ser Thr Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr  
15 20 25

ata agg aat tgg aga cgt gat gaa agc aag tgt gat cga tgc aat tgc 148  
Ile Arg Asn Trp Arg Arg Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys  
30 35 40

gcc gaa tta aga tca tcc aga tgc aca caa gct atc ttc tgc ctt aca 196  
Ala Glu Leu Arg Ser Ser Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr  
45 50 55 60

ccg gag tta tgc aca ccg agc atc tca tgt ccg aca ggt gaa tgc cgc 244  
Pro Glu Leu Cys Thr Pro Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg  
65 70 75

tgt act aag ttc cat cag tca aga tgc act aga ttc gta gaa tgc gta 292  
Cys Thr Lys Phe His Gln Ser Arg Cys Thr Arg Phe Val Glu Cys Val  
80 85 90

cct aat aag tgt aga gac gca tagaggccag ttccagcaca tacagcacca 343  
Pro Asn Lys Cys Arg Asp Ala  
95

tgatgccctg gacaatcgtg ttgttgatt gaatatgcc gtggcaggaa tctgtcctac 403  
aaaaaa 409

<210> 126  
<211> 99  
<212> PRT  
<213> Conus geographus

<400> 126

Met Asn Ile Tyr Leu Cys Leu Ala Phe Leu Leu Phe Leu Pro Ser Thr  
 1 5 10 15  
 Ile Val Asp Ser Gly Leu Leu Asp Lys Ile Glu Thr Ile Arg Asn Trp  
 20 25 30  
 Arg Arg Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys Ala Glu Leu Arg  
 35 40 45  
 Ser Ser Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Pro Glu Leu Cys  
 50 55 60  
 Thr Pro Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg Cys Thr Lys Phe  
 65 70 75 80  
 His Gln Ser Arg Cys Thr Arg Phe Val Glu Cys Val Pro Asn Lys Cys  
 85 90 95

Arg Asp Ala

<210> 127  
 <211> 65  
 <212> PRT  
 <213> Conus geographus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(65)  
 <223> Xaa at residues 2, 12, 28, 40 and 56 is Glu or gamma-carboxy-Glu;  
 Xaa at residues 27, 32, 37 and 59 is Pro or hydroxy-Pro

<400> 127  
 Asp Xaa Ser Lys Cys Asp Arg Cys Asn Cys Ala Xaa Leu Arg Ser Ser  
 1 5 10 15  
 Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Xaa Xaa Leu Cys Thr Xaa  
 20 25 30  
 Ser Ile Ser Cys Xaa Thr Gly Xaa Cys Arg Cys Thr Lys Phe His Gln  
 35 40 45  
 Ser Arg Cys Thr Arg Phe Val Xaa Cys Val Xaa Asn Lys Cys Arg Asp  
 50 55 60  
 Ala  
 65

<210> 128  
 <211> 29  
 <212> PRT  
 <213> Conus geographus  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residues 9 and 23 is Glu or gamma-carboxy-Glu; Xaa at  
 residue 28 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr  
 <400> 128

Lys Phe Leu Ser Gly Gly Phe Lys Xaa Ile Val Cys His Arg Xaa Cys  
 1 5 10 15

Ala Lys Gly Ile Ala Lys Xaa Phe Cys Asn Cys Xaa Asp  
 20 25

<210> 129  
 <211> 7  
 <212> PRT  
 <213> Conus imperialis

<220>  
 <221> PEPTIDE  
 <222> (1)..(7)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 6 is Trp  
 (D or L) or bromo-Trp (D or L)

<400> 129  
 Xaa Cys Gly Gln Ala Xaa Cys  
 1 5

<210> 130  
 <211> 524  
 <212> DNA  
 <213> Conus imperialis

<220>  
 <221> CDS  
 <222> (7)..(285)

<400> 130  
 gttaaa atg cat ctg tca ctg gca agc tca gct gct ttg atg ttg ctt 48  
 Met His Leu Ser Leu Ala Ser Ser Ala Ala Leu Met Leu Leu  
 1 5 10

ctg ctt ttt gcc ttg ggc aac ttc gtt ggg gtc cag cca gga caa ata 96  
 Leu Leu Phe Ala Leu Gly Asn Phe Val Gly Val Gln Pro Gly Gln Ile  
 15 20 25 30

aga gat ctg aac aaa gga cag ctc aag gac aac cgc cgt aac ctg caa 144  
 Arg Asp Leu Asn Lys Gly Gln Leu Lys Asp Asn Arg Arg Asn Leu Gln  
 35 40 45

tcg cag agg aaa caa atg agt ctc ctc aag tca ctt cat gat cga aat 192  
 Ser Gln Arg Lys Gln Met Ser Leu Leu Lys Ser Leu His Asp Arg Asn  
 50 55 60

ggg tgt aac ggc aac acg tgt tcc aat agc ccc tgc cct aac aac tgt 240  
 Gly Cys Asn Gly Asn Thr Cys Ser Asn Ser Pro Cys Pro Asn Asn Cys  
 65 70 75

tat tgc gat act gag gac gac tgc cac cct gac agg cgt gaa cat 285  
 Tyr Cys Asp Thr Glu Asp Asp Cys His Pro Asp Arg Arg Glu His  
 80 85 90

tagagattag agagtttctt tgtcaacatg atgtcgcacc acacctctgc tctgcagtgt 345

gtacatcgac cagtcgacgc atctgttatt tctttgtctg ttggattgta catcgaccag 405

tccacgcata tgttatttct ttgtctgttt gatttgtttt cgtgtgttca taacacacag 465

agcctttcta ttatctgtat tgcaatacac tttgcctgat aaccagaaag tccagtgc 524

<210> 131  
 <211> 93  
 <212> PRT  
 <213> Conus imperialis

<400> 131  
 Met His Leu Ser Leu Ala Ser Ser Ala Ala Leu Met Leu Leu Leu Leu  
 1 5 10 15  
 Phe Ala Leu Gly Asn Phe Val Gly Val Gln Pro Gly Gln Ile Arg Asp  
 20 25 30  
 Leu Asn Lys Gly Gln Leu Lys Asp Asn Arg Arg Asn Leu Gln Ser Gln  
 35 40 45  
 Arg Lys Gln Met Ser Leu Leu Lys Ser Leu His Asp Arg Asn Gly Cys  
 50 55 60  
 Asn Gly Asn Thr Cys Ser Asn Ser Pro Cys Pro Asn Asn Cys Tyr Cys  
 65 70 75 80  
 Asp Thr Glu Asp Asp Cys His Pro Asp Arg Arg Glu His  
 85 90

<210> 132  
 <211> 32  
 <212> PRT  
 <213> Conus imperialis

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residues 22 and 31 is Glu or gamma-carboxy-Glu; Xaa at  
 residues 13, 14 and 27 is Pro or hydroxy-Pro; Xaa at residue 18  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 132  
 Asn Gly Cys Asn Gly Asn Thr Cys Ser Asn Ser Xaa Cys Xaa Asn Asn  
 1 5 10 15  
 Cys Xaa Cys Asp Thr Xaa Asp Asp Cys His Xaa Asp Arg Arg Xaa His  
 20 25 30

<210> 133  
 <211> 350  
 <212> DNA  
 <213> Conus lacterculatus

<220>  
 <221> CDS  
 <222> (1)..(273)

<400> 133  
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cac 96  
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
                   20                                  25                                  30

ccg aag aga gag ttc cat cgt att ctg cta agg cct gac aga cag tcc 144  
 Pro Lys Arg Glu Phe His Arg Ile Leu Leu Arg Pro Asp Arg Gln Ser  
                   35                                  40                                  45

gaa acg gct tgt agg tcg ctc gga agc tac caa tgt atg ggt aaa tgc 192  
 Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly Lys Cys  
                   50                                  55                                  60

caa ctc ggg gtt cat tcc tgg tgt gaa tgc att tat aac cga ggt agt 240  
 Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg Gly Ser  
                   65                                  70                                  75                                  80

cag aag tct gga tgc gcg tgt agg tgt caa aag tgattaattg actcatttaa 293  
 Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys  
                                   85                                  90

ctcgttgaac gatttaaaaa atccagagca atatgttcga gaaaaaccga agacgac 350

<210> 134

<211> 91

<212> PRT

<213> Conus lacterculatus

<400> 134

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1                                  5                                  10                                  15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
                   20                                  25                                  30

Pro Lys Arg Glu Phe His Arg Ile Leu Leu Arg Pro Asp Arg Gln Ser  
                   35                                  40                                  45

Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly Lys Cys  
                   50                                  55                                  60

Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg Gly Ser  
                   65                                  70                                  75                                  80

Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys  
                                   85                                  90

<210> 135

<211> 45

<212> PRT

<213> Conus lacterculatus

<220>

<221> PEPTIDE

<222> (1)..(45)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 3 and 27 is  
 Glu or gamma-carboxy-Glu; Xaa at residue 25 is Trp (D or L) or  
 bromo-Trp (D or L); Xaa at residues 12 and 30 is Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 135

Xaa Ser Xaa Thr Ala Cys Arg Ser Leu Gly Ser Xaa Gln Cys Met Gly  
1 5 10 15

Lys Cys Gln Leu Gly Val His Ser Xaa Cys Xaa Cys Ile Xaa Asn Arg  
20 25 30

Gly Ser Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys  
35 40 45

&lt;210&gt; 136

&lt;211&gt; 318

&lt;212&gt; DNA

&lt;213&gt; Conus lividus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(237)

&lt;400&gt; 136

ggatcc atg aaa ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg 48  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu  
1 5 10

acg gcc agt cag ctc att aca gct gat tac tcc aga gat aag cag gag 96  
Thr Ala Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Lys Gln Glu  
15 20 25 30

tat cgt gca gag agg ctg aga gac gca atg ggg aaa ttc aaa ggt tcc 144  
Tyr Arg Ala Glu Arg Leu Arg Asp Ala Met Gly Lys Phe Lys Gly Ser  
35 40 45

agg tcg tgc gga cat agt ggt gca ggt tgt tat act cgc cct tgc tgc 192  
Arg Ser Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys  
50 55 60

cct ggt ctg cat tgc tct ggc ggc caa gct gga ggc ctg tgc gtg 237  
Pro Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val  
65 70 75

taatagtaat aatctggcgt ctgatatttc cagtctgtgc tctaccctct tttgcctgag 297

tcattccatac ctgtgctcga g 318

&lt;210&gt; 137

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Conus lividus

&lt;400&gt; 137

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Lys Gln Glu Tyr Arg  
20 25 30

Ala Glu Arg Leu Arg Asp Ala Met Gly Lys Phe Lys Gly Ser Arg Ser  
35 40 45

Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys Pro Gly



<210> 140  
 <211> 82  
 <212> PRT  
 <213> Conus lividus

<400> 140  
 Met Lys Leu Thr Cys Val Val Ile Ile Ser Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Ser Glu Phe Leu Thr Ala Asp Tyr Ser Arg Asp Lys Arg Gln Tyr Arg  
 20 25 30  
 Ala Val Arg Leu Arg Asp Ala Met Arg Asn Phe Lys Gly Thr Arg Asp  
 35 40 45  
 Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys Cys Pro  
 50 55 60  
 Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Pro Ser  
 65 70 75 80

Gly Ile

<210> 141  
 <211> 35  
 <212> PRT  
 <213> Conus lividus

<220>  
 <221> PEPTIDE  
 <222> (1)..(35)  
 <223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residues 14,  
 17 and 32 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-  
 Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 141  
 Asp Cys Gly Xaa Ser Gly Gln Gly Cys Xaa Ser Val Arg Xaa Cys Cys  
 1 5 10 15  
 Xaa Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Xaa  
 20 25 30

Ser Gly Ile  
 35

<210> 142  
 <211> 6  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is  
 Pro or hydroxy-Pro; Xaa at residue 2 is Tyr, 125I-Tyr, mono-  
 iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 142  
 Val Xaa Xaa Thr His Xaa



1                      5

<210> 143  
 <211> 6  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is  
       Pro or hydroxy-Pro; Xaa at residue 2 is Tyr, 125I-Tyr, mono-  
       iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 143  
 Arg Xaa Lys Asn Ser Xaa  
 1                      5

<210> 144  
 <211> 7  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(7)  
 <223> Xaa at residue 2 is Pro or hydroxy-Pro; Xaa at residue 6 is Trp  
       (D or L) or bromo-Trp (D or L)

<400> 144  
 Ala Arg Xaa Lys Asn Ser Xaa  
 1                      5

<210> 145  
 <211> 6  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa at residue 3 is Pro or hydroxy-Pro; Xaa at residue 7 is Trp  
       (D or L) or bromo-Trp (D or L)

<400> 145  
 Arg Xaa Lys Asn Ser Xaa  
 1                      5

<210> 146  
 <211> 360  
 <212> DNA  
 <213> Conus miles

<220>  
 <221> CDS  
 <222> (7)..(270)

<400> 146  
 ggatcc atg aaa ctg acg tgc gtg gtg atc gtc gcc gtg ctg ttc ctg  
       Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu

1	5	10	
acg gcc tgt caa ctc att act gct gcg aat tac gcc aga gat gaa cag			96
Thr Ala Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln			
15	20	25	30
gag tac ccc gct gtg agg tcg agc gac gtg atg cag gat tcc gaa gac			144
Glu Tyr Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp			
	35	40	45
ttg acg ttg acc aag aaa tgc acg gac gat tct cag ttc tgt aac cct			192
Leu Thr Leu Thr Lys Lys Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro			
	50	55	60
tcg aat cat gac tgc tgc agt ggg aag tgt atc gac gaa gga gac aac			240
Ser Asn His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn			
	65	70	75
ggc ata tgc gct ata gtc cct gaa aac tct taacaatgta tactgacatt			290
Gly Ile Cys Ala Ile Val Pro Glu Asn Ser			
80	85		
tccccctctg tgctccgccg tccgtggcct gactcgcca tccttgggcg tggatcatgaa			350
ccgctcgggtt			360
<210>	147		
<211>	88		
<212>	PRT		
<213>	Conus miles		
<400>	147		
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala			
1	5	10	15
Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln Glu Tyr			
	20	25	30
Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp Leu Thr			
	35	40	45
Leu Thr Lys Lys Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro Ser Asn			
	50	55	60
His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile			
65	70	75	80
Cys Ala Ile Val Pro Glu Asn Ser			
	85		
<210>	148		
<211>	36		
<212>	PRT		
<213>	Conus miles		
<220>			
<221>	PEPTIDE		
<222>	(1)..(36)		
<223>	Xaa at residues 23 and 34 is Glu or gamma-carboxy-Glu; Xaa at residues 10 and 33 is Pro or hydroxy-Pro		

&lt;400&gt; 148

Cys Thr Asp Asp Ser Gln Phe Cys Asn Xaa Ser Asn His Asp Cys Cys  
 1 5 10 15

Ser Gly Lys Cys Ile Asp Xaa Gly Asp Asn Gly Ile Cys Ala Ile Val  
 20 25 30

Xaa Xaa Asn Ser  
 35

&lt;210&gt; 149

&lt;211&gt; 357

&lt;212&gt; DNA

&lt;213&gt; Conus miles

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(270)

&lt;400&gt; 149

ggatcc atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ttc ctg 48  
 Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu  
 1 5 10

acg gcc tgt caa ctc att act gct gcg aat tac gcc aga gat gaa cag 96  
 Thr Ala Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln  
 15 20 25 30

gag tac cct gct gtg agg tcg agc gac gtg atg cag gat tcc gaa gac 144  
 Glu Tyr Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp  
 35 40 45

ctg acg ttg acc aag aaa tgc acg gag gat tct cag ttc tgt aac cct 192  
 Leu Thr Leu Thr Lys Lys Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro  
 50 55 60

tcg aat cat gac tgc tgc agt ggg aag tgt atc gac gaa gga gac aac 240  
 Ser Asn His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn  
 65 70 75

ggc ata tgc gct ata gtc cct gaa aac tct taacaatgta tactgacatt 290  
 Gly Ile Cys Ala Ile Val Pro Glu Asn Ser  
 80 85

tccccctctg tgctccgcgcg tccgtggcct gactcgcca tccttgggcg tggatcatgaa 350

ccgctcg 357

&lt;210&gt; 150

&lt;211&gt; 88

&lt;212&gt; PRT

&lt;213&gt; Conus miles

&lt;400&gt; 150

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Ala Asn Tyr Ala Arg Asp Glu Gln Glu Tyr  
 20 25 30

Pro Ala Val Arg Ser Ser Asp Val Met Gln Asp Ser Glu Asp Leu Thr  
35 40 45

Leu Thr Lys Lys Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro Ser Asn  
50 55 60

His Asp Cys Cys Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile  
65 70 75 80

Cys Ala Ile Val Pro Glu Asn Ser  
85

<210> 151

<211> 36

<212> PRT

<213> Conus miles

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residues 3, 23 and 34 is Glu or gamma-carboxy-Glu; Xaa at residues 10 and 33 is Pro or hydroxy-Pro

<400> 151

Cys Thr Xaa Asp Ser Gln Phe Cys Asn Xaa Ser Asn His Asp Cys Cys  
1 5 10 15

Ser Gly Lys Cys Ile Asp Xaa Gly Asp Asn Gly Ile Cys Ala Ile Val  
20 25 30

Xaa Xaa Asn Ser  
35

<210> 152

<211> 327

<212> DNA

<213> Conus miliaris

<220>

<221> CDS

<222> (12)..(239)

<400> 152

ggatccatga a ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg acg 50  
Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr  
1 5 10

gcc tgt caa ctc act aca gct gtg act tcc tcc aga ggt caa cag aag 98  
Ala Cys Gln Leu Thr Thr Ala Val Thr Ser Ser Arg Gly Gln Gln Lys  
15 20 25

cat cgt gct ctg agg tca act gac aaa aac tcc agg atg acc aag cgt 146  
His Arg Ala Leu Arg Ser Thr Asp Lys Asn Ser Arg Met Thr Lys Arg  
30 35 40 45

tgc acg cct cca ggt gga ctc tgt tac cat gct tat ccc tgc tgc agc 194  
Cys Thr Pro Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser  
50 55 60

aag act tgc aat ctc gat acc agc caa tgt gag cct agg tgg tca 239  
Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser  
65 70 75

tgaaccactc aataccctct cctctggagg cttcagagga actacattga aataaaaaccg 299

cattgcaacg aaaaaaaaaa aaaaaaaaaa 327

<210> 153

<211> 76

<212> PRT

<213> Conus miliaris

<400> 153

Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala Cys Gln  
1 5 10 15

Leu Thr Thr Ala Val Thr Ser Ser Arg Gly Gln Gln Lys His Arg Ala  
20 25 30

Leu Arg Ser Thr Asp Lys Asn Ser Arg Met Thr Lys Arg Cys Thr Pro  
35 40 45

Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser Lys Thr Cys  
50 55 60

Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser  
65 70 75

<210> 154

<211> 31

<212> PRT

<213> Conus miliaris

 $\langle 220 \rangle$ 

<221> PEPTIDE

<222> (1) .. (31)

<223> Xaa at residue 27 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 4, 13 and 28 is Pro or hydroxy-Pro; Xaa at residue 30 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 9 and 12 is Tyr, 125 I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 154

Cys Thr Xaa Xaa Gly Gly Leu Cys Xaa His Ala Xaa Xaa Cys Cys Ser  
1 5 10 15

Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Xaa Xaa Arg Xaa Ser  
20 25 30

<210> 155

<211> 193

<212> DNA

<213> Conus monachus

<220>

<221> CDS

 $\langle 222 \rangle \quad (28) \dots (162)$ 

<400> 155

tgtgtgtgtg tqgtttctggg tccagca tct gat gtc agg aat gcc gca gtc cac 54

Ser Asp Val Arg Asn Ala Ala Val His  
1 5

gaa aga cag aag gat ctg gtc gtt acg gcc acc acg act tgc tgt ggt 102  
Glu Arg Gln Lys Asp Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly  
10 15 20 25

tat aat ccg atg aca atg tgc cct cct tgc atg tgc act aat acc tgc 150  
Tyr Asn Pro Met Thr Met Cys Pro Pro Cys Met Cys Thr Asn Thr Cys  
30 35 40

aaa aaa agt ggc tgatgctcca ggaccctctg aaccacgacg t 193  
Lys Lys Ser Gly  
45

<210> 156  
<211> 45  
<212> PRT  
<213> Conus monachus

<400> 156  
Ser Asp Val Arg Asn Ala Ala Val His Glu Arg Gln Lys Asp Leu Val  
1 5 10 15

Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asn Pro Met Thr Met Cys  
20 25 30

Pro Pro Cys Met Cys Thr Asn Thr Cys Lys Lys Ser Gly  
35 40 45

<210> 157  
<211> 33  
<212> PRT  
<213> Conus monachus

<220>  
<221> PEPTIDE  
<222> (1)..(33)  
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 17, 22 and  
23 is Pro or hydroxy-Pro; Xaa at residue 15 is Tyr, 125I-Tyr,  
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 157  
Xaa Lys Asp Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asn  
1 5 10 15

Xaa Met Thr Met Cys Xaa Xaa Cys Met Cys Thr Asn Thr Cys Lys Lys  
20 25 30

Ser

<210> 158  
<211> 350  
<212> DNA  
<213> Conus monachus

<220>  
<221> CDS  
<222> (1)..(282)

<400> 158  
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca agc 96  
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser  
 20 25 30

ctg aag agc gac ttc tat cgt gct ctg aga ggg tat gac aga cag tgc 144  
 Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Gly Tyr Asp Arg Gln Cys  
 35 40 45

act ctt gtc aac aat tgt gac cgg aac ggt gag cgt gcg tgt aac ggt 192  
 Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys Asn Gly  
 50 55 60

gat tgc tct tgc gag ggc cag att tgt aaa tgc ggt tat aga gtc agt 240  
 Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg Val Ser  
 65 70 75 80

cct ggg aag tca gga tgc gcg tgt act tgt aga aat gcc aaa 282  
 Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
 85 90

tgaatcattt aactcgttga aagattttttt aaaaatccag agctatatgt tcgagaaaaa 342

ccgaagac 350

<210> 159  
 <211> 94  
 <212> PRT  
 <213> Conus monachus

<400> 159  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser  
 20 25 30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Gly Tyr Asp Arg Gln Cys  
 35 40 45

Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys Asn Gly  
 50 55 60

Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg Val Ser  
 65 70 75 80

Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
 85 90

<210> 160  
 <211> 48  
 <212> PRT  
 <213> Conus monachus

<220>  
 <221> PEPTIDE

<222> (1)..(48)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 13 and 23 is Glu or gamma-carboxy-Glu; Xaa at residue 35 is Pro or hydroxy-Pro; Xaa at residue 31 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 160

Xaa Cys Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Xaa Arg Ala Cys  
1 5 10 15

Asn Gly Asp Cys Ser Cys Xaa Gly Gln Ile Cys Lys Cys Gly Xaa Arg  
20 25 30

Val Ser Xaa Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
35 40 45

<210> 161

<211> 211

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(192)

<400> 161

atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48  
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

gca cct agc gtt gat gcc aaa gtt cat ctg aag acc aaa ggt gat ggg 96  
Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly  
20 25 30

ccc ctg tca tct ttc cga gat aat gca aag agt acc cta caa aga ctt 144  
Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu  
35 40 45

cag gac aaa agc act tgc tgt ggc ttt aag atg tgt att cct tgt cgt 192  
Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg  
50 55 60

taaccagcat gaaggatcc 211

<210> 162

<211> 64

<212> PRT

<213> Conus pennaceus

<400> 162

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly  
20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu  
35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg



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50                               55                               60

<210> 163
<211> 13
<212> PRT
<213> Conus pennaceus

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 163
Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Arg
1          5          10

<210> 164
<211> 450
<212> DNA
<213> Conus pennaceus

<220>
<221> CDS
<222> (1)..(234)

<400> 164
atg ttg ctt ctg ctg ttt gcc ttg ggc agc ttc gtt gtg gtc cag tca      48
Met Leu Leu Leu Leu Phe Ala Leu Gly Ser Phe Val Val Val Gln Ser
1          5          10          15

gga cag ata aca aga gat gtg gac aat ggg cag ctc gcg gac aac cgc      96
Gly Gln Ile Thr Arg Asp Val Asp Asn Gly Gln Leu Ala Asp Asn Arg
          20          25          30

cgt acc ctg cga tcg cag tgg aag caa gtg agt ttc ttc aag tca ctt      144
Arg Thr Leu Arg Ser Gln Trp Lys Gln Val Ser Phe Phe Lys Ser Leu
          35          40          45

gat aaa cga ctg act tgt aac gat oct tgc cag atg cat tcc gat tgc      192
Asp Lys Arg Leu Thr Cys Asn Asp Pro Cys Gln Met His Ser Asp Cys
          50          55          60

ggc ata tgt gaa tgc gtg gaa aat aaa tgc ata ttt ttc atg      234
Gly Ile Cys Glu Cys Val Glu Asn Lys Cys Ile Phe Phe Met
65          70          75

taaacggatt gagtttgctt gtcaacacaa tgtcgcactg cagctcttct ctaccggtgg      294

gtacatcgac caaacgacgc atcttttatt tctttgtctg tttcgtttgt tctcctgtgt      354

tcataacgta cagagccctt taactaccct tactgctctt cacttaacct gataacctga      414

aggtcggtg cagctggcgt agccttcaca gtttcg      450

<210> 165
<211> 78
<212> PRT
<213> Conus pennaceus

<400> 165

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Met Leu Leu Leu Leu Phe Ala Leu Gly Ser Phe Val Val Val Gln Ser  
1 5 10 15

Gly Gln Ile Thr Arg Asp Val Asp Asn Gly Gln Leu Ala Asp Asn Arg  
20 25 30

Arg Thr Leu Arg Ser Gln Trp Lys Gln Val Ser Phe Phe Lys Ser Leu  
35 40 45

Asp Lys Arg Leu Thr Cys Asn Asp Pro Cys Gln Met His Ser Asp Cys  
50 55 60

Gly Ile Cys Glu Cys Val Glu Asn Lys Cys Ile Phe Phe Met  
65 70 75

<210> 166

<211> 27

<212> PRT

<213> Conus pennaceus

<220>

<221> PEPTIDE

<222> (1)..(27)

<223> Xaa at residues 17 and 20 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro

<400> 166

Leu Thr Cys Asn Asp Xaa Cys Gln Met His Ser Asp Cys Gly Ile Cys  
1 5 10 15

Xaa Cys Val Xaa Asn Lys Cys Ile Phe Phe Met  
20 25

<210> 167

<211> 413

<212> DNA

<213> Conus pulicarius

<220>

<221> CDS

<222> (1)..(243)

<400> 167

atg aaa ctg acg tgt gtg gtg atc gtc gcc gtg ctg ttc ctg acg gcc 48  
Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

tgt caa ctc agt aca gct gat gac tcc aga gat gag cag cag gat cct 96  
Cys Gln Leu Ser Thr Ala Asp Asp Ser Arg Asp Glu Gln Gln Asp Pro  
20 25 30

ttg gtg agg tcg cat cgt gag gag cag aaa gcc gag gac ccc aag acg 144  
Leu Val Arg Ser His Arg Glu Glu Gln Lys Ala Glu Asp Pro Lys Thr  
35 40 45

gcc gag aga tgt tca gat ttc gga tcc gac tgt gtt cct gct act cat 192  
Ala Glu Arg Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His  
50 55 60

aac tgc tgc agt ggt gaa tgt ttt ggc ttc gag gac ttc ggc tta tgc 240

Asn Cys Cys Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys  
65 70 75 80

acg taaaactggg ctgacgtctg atattccccc ctctgtcctt catcctcttt 293  
Thr

tgccatgattc atccatacct atatgtgctc ctgaaccgct gtgtaccttt accctgggtgg 353

cttcagagga cgttatatca aaataaaacc gcgttgcaat gacaaaaaaaa aaaaaaaaaa 413

<210> 168

<211> 81

<212> PRT

<213> Conus pulicarius

<400> 168

Met Lys Leu Thr Cys Val Val Ile Val Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Leu Ser Thr Ala Asp Asp Ser Arg Asp Glu Gln Gln Asp Pro  
20 25 30

Leu Val Arg Ser His Arg Glu Glu Gln Lys Ala Glu Asp Pro Lys Thr  
35 40 45

Ala Glu Arg Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His  
50 55 60

Asn Cys Cys Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys  
65 70 75 80

Thr

<210> 169

<211> 30

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> Xaa at residues 19 and 24 is Glu or gamma-carboxy-Glu; Xaa at  
residue 10 is Pro or hydroxy-Pro

<400> 169

Cys Ser Asp Phe Gly Ser Asp Cys Val Xaa Ala Thr His Asn Cys Cys  
1 5 10 15

Ser Gly Xaa Cys Phe Gly Phe Xaa Asp Phe Gly Leu Cys Thr  
20 25 30

<210> 170

<211> 375

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

&lt;222&gt; (24)..(260)

&lt;400&gt; 170

gacaggattg aacaaaattc agg atg tca aga ttt gga atc atg gtg cta acc 53  
 Met Ser Arg Phe Gly Ile Met Val Leu Thr  
 1 5 10

ttt cta ctt ctt gtg tcc atg gca acc agc cat cgt tat gca aga ggg 101  
 Phe Leu Leu Leu Val Ser Met Ala Thr Ser His Arg Tyr Ala Arg Gly  
 15 20 25

aag cag gcg acg cga agg aac gca atc aac atc aga cgg aga agc aca 149  
 Lys Gln Ala Thr Arg Arg Asn Ala Ile Asn Ile Arg Arg Arg Ser Thr  
 30 35 40

cca aaa act gag gcg tgc gaa gag gtc tgt gag ctg gaa gaa aag cac 197  
 Pro Lys Thr Glu Ala Cys Glu Glu Val Cys Glu Leu Glu Glu Lys His  
 45 50 55

tgc tgc tgc ata aga agt gac gga ccc aaa tgt tcc cgt aag tgc ctg 245  
 Cys Cys Cys Ile Arg Ser Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu  
 60 65 70

ttg tca atc ttc tgt tagtttctgt acactgtctc attcattatc ttatcagttac 300  
 Leu Ser Ile Phe Cys  
 75

aagtgtaaac gagacatgtc agaaagtcga aggttgtgctg taatttgata agtattgttt 360

gctgggatga acgga 375

&lt;210&gt; 171

&lt;211&gt; 79

&lt;212&gt; PRT

&lt;213&gt; Conus purpurascens

&lt;400&gt; 171

Met Ser Arg Phe Gly Ile Met Val Leu Thr Phe Leu Leu Leu Val Ser  
 1 5 10 15

Met Ala Thr Ser His Arg Tyr Ala Arg Gly Lys Gln Ala Thr Arg Arg  
 20 25 30

Asn Ala Ile Asn Ile Arg Arg Arg Ser Thr Pro Lys Thr Glu Ala Cys  
 35 40 45

Glu Glu Val Cys Glu Leu Glu Glu Lys His Cys Cys Cys Ile Arg Ser  
 50 55 60

Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu Leu Ser Ile Phe Cys  
 65 70 75

&lt;210&gt; 172

&lt;211&gt; 37

&lt;212&gt; PRT

&lt;213&gt; Conus purpurascens

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(37)

<223> Xaa at residues 4, 7, 8, 11, 13 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 3 and 25 is Pro or hydroxy-Pro

<400> 172

Xaa	Lys	Thr	Xaa	Ala	Cys	Xaa	Xaa	Val	Cys	Xaa	Leu	Xaa	Xaa	Lys	His
1				5					10					15	
Cys	Cys	Cys	Ile	Arg	Ser	Asp	Gly	Xaa	Lys	Cys	Ser	Arg	Lys	Cys	Leu
			20					25					30		

Leu	Ser	Ile	Phe	Cys
				35

<210> 173

<211> 373

<212> DNA

<213> *Conus purpurascens*

<220>

<221> CDS

<222> (24)..(260)

<400> 173

gacag	gattg	aacaaa	attc	agg	atg	tca	gga	ttg	gga	atc	atg	gtg	cta	acc	53
					Met	Ser	Gly	Leu	Gly	Ile	Met	Val	Leu	Thr	
					1				5					10	

ctt	cta	ctt	ctt	gtg	tcc	atg	gca	acc	aac	cat	cag	gat	aga	gga	gag	101
Leu	Leu	Leu	Leu	Val	Ser	Met	Ala	Thr	Asn	His	Gln	Asp	Arg	Gly	Glu	
				15					20					25		

aag	cag	gtg	acg	caa	agg	gac	gca	atc	aac	gtc	aga	cgg	aga	aga	tca	149
Lys	Gln	Val	Thr	Gln	Arg	Asp	Ala	Ile	Asn	Val	Arg	Arg	Arg	Arg	Ser	
			30					35					40			

atc	acc	cag	caa	gtc	gta	tct	gag	gag	tgc	aaa	aag	tac	tgt	aag	aaa	197
Ile	Thr	Gln	Gln	Val	Val	Ser	Glu	Glu	Cys	Lys	Lys	Tyr	Cys	Lys	Lys	
		45					50					55				

cag	aac	aag	aat	tgc	tgc	agc	agt	aaa	cat	gaa	gaa	ccc	aga	tgt	gcc	245
Gln	Asn	Lys	Asn	Cys	Cys	Ser	Ser	Lys	His	Glu	Glu	Pro	Arg	Cys	Ala	
	60					65				70						

aag	ata	tgc	ttc	gga	tagttt	ctgt	acacgg	tctc	attcatt	att	ttatc	agtac				300
Lys	Ile	Cys	Phe	Gly												
																75

aag	ttaa	acg	agac	ctat	ca	gaag	tcga	ag	gtt	gtgc	ata	attt	gata	aaa	catt	gttt	gc	360
-----	------	-----	------	------	----	------	------	----	-----	------	-----	------	------	-----	------	------	----	-----

tgg	gat	gaac	gga															373
-----	-----	------	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	-----

<210> 174

<211> 79

<212> PRT

<213> *Conus purpurascens*

<400> 174

Met	Ser	Gly	Leu	Gly	Ile	Met	Val	Leu	Thr	Leu	Leu	Leu	Leu	Val	Ser
1				5					10					15	

Met	Ala	Thr	Asn	His	Gln	Asp	Arg	Gly	Glu	Lys	Gln	Val	Thr	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20 25 30  
 Asp Ala Ile Asn Val Arg Arg Arg Arg Ser Ile Thr Gln Gln Val Val  
           35                          40                          45

Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys Gln Asn Lys Asn Cys Cys  
       50                          55                          60  
 Ser Ser Lys His Glu Glu Pro Arg Cys Ala Lys Ile Cys Phe Gly  
       65                          70                          75

<210> 175  
 <211> 32  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residues 4, 5, 23 and 24 is Glu or gamma-carboxy-Glu; Xaa  
       at residue 25 is Pro or hydroxy-Pro; Xaa at residue 9 is Tyr,  
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
       O-phospho-Tyr

<400> 175  
 Val Val Ser Xaa Xaa Cys Lys Lys Xaa Cys Lys Lys Gln Asn Lys Asn  
   1                          5                          10                          15

Cys Cys Ser Ser Lys His Xaa Xaa Xaa Arg Cys Ala Lys Ile Cys Phe  
           20                          25                          30

<210> 176  
 <211> 24  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residue 8 is Glu or gamma-carboxy-Glu; Xaa at residue 12  
       is Pro or hydroxy-Pro; Xaa at residue 22 is Tyr, 125I-Tyr, mono-  
       iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 176  
 Asp Cys Cys Gly Val Lys Leu Xaa Met Cys His Xaa Cys Leu Cys Asp  
   1                          5                          10                          15

Asn Ser Cys Lys Asn Xaa Gly Lys  
           20

<210> 177  
 <211> 235  
 <212> DNA  
 <213> Conus purpurascens

<220>  
 <221> CDS  
 <222> (1)..(204)

<400> 177  
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 ttc act tca gat cgt gca tcg gat gac agg aat acc aac gac aaa gca 96  
 Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala  
 20 25 30  
 tct cgc ctg ctc tct cac gtt gtc agg gga tgc tgt ggt agc tat ccc 144  
 Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Ser Tyr Pro  
 35 40 45  
 aat gct gcc tgt cat cct tgc ggt tgt aaa gat agg cca tcg tat tgt 192  
 Asn Ala Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys  
 50 55 60  
 ggt caa gga cgc tgatgctcca ggaccctctg aaccacgacg t 235  
 Gly Gln Gly Arg  
 65

<210> 178  
 <211> 68  
 <212> PRT  
 <213> Conus purpurascens

<400> 178  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 Phe Thr Ser Asp Arg Ala Ser Asp Asp Arg Asn Thr Asn Asp Lys Ala  
 20 25 30  
 Ser Arg Leu Leu Ser His Val Val Arg Gly Cys Cys Gly Ser Tyr Pro  
 35 40 45  
 Asn Ala Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys  
 50 55 60  
 Gly Gln Gly Arg  
 65

<210> 179  
 <211> 25  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residues 7, 13 and 20 is Pro or hydroxy-Pro; Xaa at  
 residues 6 and 22 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-  
 Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 179  
 Gly Cys Cys Gly Ser Xaa Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys  
 1 5 10 15  
 Lys Asp Arg Xaa Ser Xaa Cys Gly Gln  
 20 25

<210> 180

<211> 229  
 <212> DNA  
 <213> *Conus purpurascens*

<220>  
 <221> CDS  
 <222> (1)..(198)

<400> 180  
 atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc gtt tcc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 ttc acc gta gat cgt gca act gat ggc agg agt gct gca gcc ata gcg 96  
 Phe Thr Val Asp Arg Ala Thr Asp Gly Arg Ser Ala Ala Ala Ile Ala  
 20 25 30  
 ttt gcc ctg atc gct ccg acc gtc cgg gaa gga tgc tgt tct aat cct 144  
 Phe Ala Leu Ile Ala Pro Thr Val Arg Glu Gly Cys Cys Ser Asn Pro  
 35 40 45  
 gcc tgt cat cct tgc ggt tgt aaa gat agg cca tcg tat tgt ggt caa 192  
 Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys Gly Gln  
 50 55 60  
 gga cgc tgatgctcca ggaccctctg aaccacgacg t 229  
 Gly Arg  
 65

<210> 181  
 <211> 66  
 <212> PRT  
 <213> *Conus purpurascens*

<400> 181  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 Phe Thr Val Asp Arg Ala Thr Asp Gly Arg Ser Ala Ala Ala Ile Ala  
 20 25 30  
 Phe Ala Leu Ile Ala Pro Thr Val Arg Glu Gly Cys Cys Ser Asn Pro  
 35 40 45  
 Ala Cys His Pro Cys Gly Cys Lys Asp Arg Pro Ser Tyr Cys Gly Gln  
 50 55 60  
 Gly Arg  
 65

<210> 182  
 <211> 23  
 <212> PRT  
 <213> *Conus purpurascens*

<220>  
 <221> PEPTIDE  
 <222> (1)..(23)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residues 7,  
 11 and 18 is Pro or hydroxy-Pro; Xaa at residue 20 is Tyr, 125I-



Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 182

Xaa Gly Cys Cys Ser Asn Xaa Ala Cys His Xaa Cys Gly Cys Lys Asp  
1 5 10 15

Arg Xaa Ser Xaa Cys Gly Gln  
20

<210> 183

<211> 334

<212> DNA

<213> *Conus purpurascens*

<220>

<221> CDS

<222> (1)..(261)

<400> 183

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48  
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
1 5 10 15

ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96  
Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg  
20 25 30

ctg acg agg gac ttc tat cgt act ctg cca gtg tct act aga gga tgc 144  
Leu Thr Arg Asp Phe Tyr Arg Thr Leu Pro Val Ser Thr Arg Gly Cys  
35 40 45

agc ggc tcc cct tgt ttt aaa aac aaa acg tgt cgg gat gaa tgc ata 192  
Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu Cys Ile  
50 55 60

tgc ggc ggc tta tcc aat tgt tgg tgt ggc tac ggc ggt agt cga gga 240  
Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser Arg Gly  
65 70 75 80

tgc aag tgt aca tgt aga gag tgattaatcg actctttaac tcgttgaatt 291  
Cys Lys Cys Thr Cys Arg Glu  
85

atttaaaaaa tccagagcaa tatgttcgag aaaaaccgaa gac 334

<210> 184

<211> 87

<212> PRT

<213> *Conus purpurascens*

<400> 184

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg  
20 25 30

Leu Thr Arg Asp Phe Tyr Arg Thr Leu Pro Val Ser Thr Arg Gly Cys  
35 40 45

Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu Cys Ile  
50 55 60

Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser Arg Gly  
65 70 75 80

Cys Lys Cys Thr Cys Arg Glu  
85

<210> 185

<211> 41

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(41)

<223> Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 26 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 185

Gly Cys Ser Gly Ser Xaa Cys Phe Lys Asn Lys Thr Cys Arg Asp Xaa  
1 5 10 15

Cys Ile Cys Gly Gly Leu Ser Asn Cys Xaa Cys Gly Xaa Gly Gly Ser  
20 25 30

Arg Gly Cys Lys Cys Thr Cys Arg Xaa  
35 40

<210> 186

<211> 327

<212> DNA

<213> Conus purpurascens

<220>

<221> CDS

<222> (29)..(256)

<400> 186

cgacctcaag agggatcgat agcagttc atg atg tct aaa ctg gga gcc ttg 52  
Met Met Ser Lys Leu Gly Ala Leu  
1 5

ttg acc atc tgt ctg ctt ctg ttt ccc att act gct ctt ctg atg gat 100  
Leu Thr Ile Cys Leu Leu Leu Phe Pro Ile Thr Ala Leu Leu Met Asp  
10 15 20

gga gat caa cct gca gac cga cct gca gaa cgt atg gat tac gac att 148  
Gly Asp Gln Pro Ala Asp Arg Pro Ala Glu Arg Met Asp Tyr Asp Ile  
25 30 35 40

tca tct gag gtg cat cgt ttg ctt gaa agg aga cac ccg ccc tgt tgc 196  
Ser Ser Glu Val His Arg Leu Leu Glu Arg Arg His Pro Pro Cys Cys  
45 50 55

atg tac ggc aga tgc cgt cga tat ccc gga tgc tct agt gcc tct tgt 244

Met Tyr Gly Arg Cys Arg Arg Tyr Pro Gly Cys Ser Ser Ala Ser Cys  
                   60                                  65                                  70

tgc cag gga gga taacgtgttg atgaccaact ttgttacacg gctacgtcaa 296  
 Cys Gln Gly Gly  
                   75

gtgtctactg aataagtaaa acgattgcag t 327

<210> 187  
 <211> 76  
 <212> PRT  
 <213> Conus purpurascens

<400> 187  
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe  
 1                  5                                  10                                  15

Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro  
                   20                                  25                                  30

Ala Glu Arg Met Asp Tyr Asp Ile Ser Ser Glu Val His Arg Leu Leu  
                   35                                  40                                  45

Glu Arg Arg His Pro Pro Cys Cys Met Tyr Gly Arg Cys Arg Arg Tyr  
                   50                                  55                                  60

Pro Gly Cys Ser Ser Ala Ser Cys Cys Gln Gly Gly  
 65                                  70                                  75

<210> 188  
 <211> 24  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residues 2, 3 and 14 is Pro or hydroxy-Pro; Xaa at residue  
           residues 7 and 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
           O-sulpho-Tyr or O-phospho-Tyr

<400> 188  
 His Xaa Xaa Cys Cys Met Xaa Gly Arg Cys Arg Arg Xaa Xaa Gly Cys  
 1                  5                                  10                                  15

Ser Ser Ala Ser Cys Cys Gln Gly  
                   20

<210> 189  
 <211> 24  
 <212> PRT  
 <213> Conus purpurascens

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residues 2, 3, 12 and 14 is Pro or hydroxy-Pro; Xaa at  
           residues 7 and 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
           O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 189

Gly Xaa Xaa Cys Cys Leu Xaa Gly Ser Cys Arg Xaa Phe Xaa Gly Cys  
 1 5 10 15

Xaa Asn Ala Leu Cys Cys Arg Lys  
 20

&lt;210&gt; 190

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Conus quercinus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(237)

&lt;400&gt; 190

ggatcc atg aaa ctg acg tgc gtg gtg atc atc gcc gtg ctg ttt ctg 48  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu  
 1 5 10

aca gcc agt cag ctc gtt aca gct gat tac acc aga gat aaa tgg caa 96  
 Thr Ala Ser Gln Leu Val Thr Ala Asp Tyr Thr Arg Asp Lys Trp Gln  
 15 20 25 30

tac cct gca gcg agt ttg aga ggc gga atg tgg aat ttg aga gat acc 144  
 Tyr Pro Ala Ala Ser Leu Arg Gly Gly Met Trp Asn Leu Arg Asp Thr  
 35 40 45

agg gcg tgc tcg caa gta ggt gaa gct tgt ttt cct cag aaa cct tgc 192  
 Arg Ala Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys  
 50 55 60

tgc cct gga ttc ctt tgc aat cac atc gga ggc atg tgc cac cac 237  
 Cys Pro Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His  
 65 70 75

tagtaacagt ctggcatctg atatttcccc tctgcgctcc accctctttt ggctgattca 297

tccttacctg tgtgtggtca tgaaccactc agtagctaca cctctggtgg cttcagagga 357

cgtatatcaa aataaaacca cattgcaaaa aaaaaaaaaa aaa 400

&lt;210&gt; 191

&lt;211&gt; 77

&lt;212&gt; PRT

&lt;213&gt; Conus quercinus

&lt;400&gt; 191

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
 1 5 10 15

Ser Gln Leu Val Thr Ala Asp Tyr Thr Arg Asp Lys Trp Gln Tyr Pro  
 20 25 30

Ala Ala Ser Leu Arg Gly Gly Met Trp Asn Leu Arg Asp Thr Arg Ala  
 35 40 45

Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys Cys Pro



Gly Glu Thr Tyr Gln Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe  
50 55 60

gac ctg gct aca tgc acc gtc gcg ggc tgc aca ggc ttt gga ccc gag 241  
Asp Leu Ala Thr Cys Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu  
65 70 75 80

tgattggtac tattccacac ctagcaatgt tcacactgga accggaactt gatactacct 301

tctaaatata atcaatttgt ttcaaaaaggc ccaaa 336

<210> 195  
<211> 80  
<212> PRT  
<213> *Conus radiatus*

<400> 195  
Met Asn Cys Leu Val Leu Ala Leu Val Thr Ile Gly Leu Leu Ala Ala  
1 5 10 15

Thr Thr Ala Ala Pro Leu Asp Thr Thr Thr Val Leu Leu Ser Thr Thr  
20 25 30

Thr Arg Asp Val Lys Gly Cys Val Tyr Glu Gly Ile Glu Tyr Ser Val  
35 40 45

Gly Glu Thr Tyr Gln Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe  
50 55 60

Asp Leu Ala Thr Cys Thr Val Ala Gly Cys Thr Gly Phe Gly Pro Glu  
65 70 75 80

<210> 196  
<211> 43  
<212> PRT  
<213> *Conus radiatus*

<220>  
<221> PEPTIDE  
<222> (1)..(43)  
<223> Xaa at residues 5, 8, 13 and 43 is Glu or gamma-carboxy-Glu; Xaa  
at residue 42 is Pro or hydroxy-Pro; Xaa at residues 4,9 and 15  
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
or O-phospho-Tyr

<400> 196  
Gly Cys Val Xaa Xaa Gly Ile Xaa Xaa Ser Val Gly Xaa Thr Xaa Gln  
1 5 10 15

Ala Asp Cys Asn Thr Cys Arg Cys Asp Gly Phe Asp Leu Ala Thr Cys  
20 25 30

Thr Val Ala Gly Cys Thr Gly Phe Gly Xaa Xaa  
35 40

<210> 197  
<211> 536  
<212> DNA  
<213> *Conus radiatus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (87)..(296)

&lt;400&gt; 197

gtgagagtcc aacagcccaa acctttcaac tcactatgtg gcagttgcag ttttcaacgt 60

ctggacagga ttcaacaaaa ttcagg atg tca gga ttg gga atc atg gtg cta 113  
 Met Ser Gly Leu Gly Ile Met Val Leu  
 1 5

acc ctt cta ctt ctt gtg tcc atg gca acc agt cgt cag gat aga gga 161  
 Thr Leu Leu Leu Leu Val Ser Met Ala Thr Ser Arg Gln Asp Arg Gly  
 10 15 20 25

gtg gga cag ctg atg cca cgc gtc tcg ttc aaa gcc tgc aaa tca aat 209  
 Val Gly Gln Leu Met Pro Arg Val Ser Phe Lys Ala Cys Lys Ser Asn  
 30 35 40

tat gat tgc ccc cag cgt ttc aaa tgc tgc agt tac acc tgg aat gga 257  
 Tyr Asp Cys Pro Gln Arg Phe Lys Cys Cys Ser Tyr Thr Trp Asn Gly  
 45 50 55

tcc agt gga tac tgt aaa cgt gtt tgc tat ctt tat cgt tagtgtaata 306  
 Ser Ser Gly Tyr Cys Lys Arg Val Cys Tyr Leu Tyr Arg  
 60 65 70

cacaaagtga ctctgttcat tcctctccat catctcttta gaaacaacac ggtgtcgaga 366

tcgtttcttt gtgatgaaga gtagtatcac gggcagagtt cactagagat ctcaaata 426

aaacaagatt atttagtaag ttggggaaaa tctggatctc gaaaagattc cttgaaaact 486

ccgtatttaa cacgcttgag agatgataat aaagaattct gaaagacaaa 536

&lt;210&gt; 198

&lt;211&gt; 70

&lt;212&gt; PRT

&lt;213&gt; Conus radiatus

&lt;400&gt; 198

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser  
 1 5 10 15

Met Ala Thr Ser Arg Gln Asp Arg Gly Val Gly Gln Leu Met Pro Arg  
 20 25 30

Val Ser Phe Lys Ala Cys Lys Ser Asn Tyr Asp Cys Pro Gln Arg Phe  
 35 40 45

Lys Cys Cys Ser Tyr Thr Trp Asn Gly Ser Ser Gly Tyr Cys Lys Arg  
 50 55 60

Val Cys Tyr Leu Tyr Arg  
 65 70

&lt;210&gt; 199

&lt;211&gt; 34

&lt;212&gt; PRT

&lt;213&gt; Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residue 9 is Pro or hydroxy-Pro; Xaa at residue 19 is Trp  
 (D or L) or bromo-Trp (D or L); Xaa at residues 6, 17 and 33 is  
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 199  
 Ala Cys Lys Ser Asn Xaa Asp Cys Xaa Gln Arg Phe Lys Cys Cys Ser  
 1 5 10 15  
 Xaa Thr Xaa Asn Gly Ser Ser Gly Xaa Cys Lys Arg Val Cys Xaa Leu  
 20 25 30  
 Xaa Arg

<210> 200  
 <211> 356  
 <212> DNA  
 <213> *Conus radiatus*

<220>  
 <221> CDS  
 <222> (1)..(279)

<400> 200  
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1 5 10 15  
 ctg gca tcc agc cag cag gaa gga gat gtc cag gca agg aaa aca cac 96  
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
 20 25 30  
 ccg aag aga gag ttc caa cgt att ctg cta agg tct ggc aga aag tgc 144  
 Pro Lys Arg Glu Phe Gln Arg Ile Leu Leu Arg Ser Gly Arg Lys Cys  
 35 40 45  
 aat ttc gac aaa tgt aaa ggt acc gga gtc tac aat tgt ggg gaa tcc 192  
 Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly Glu Ser  
 50 55 60  
 tgc tca tgc gaa ggt ttg cac agt tgt cgc tgc act tat aac atc ggt 240  
 Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn Ile Gly  
 65 70 75 80  
 tct atg aag tct gga tgc gcg tgt att tgt aca tac tat taatgattaa 289  
 Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr  
 85 90  
 ttgactcggtt taactcggtt aacgatttaa aaaatccaga gcaatatggt cgagaaaaac 349  
 cgaagac 356

<210> 201  
 <211> 93  
 <212> PRT  
 <213> *Conus radiatus*



&lt;400&gt; 201

Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr His  
 20 25 30

Pro Lys Arg Glu Phe Gln Arg Ile Leu Leu Arg Ser Gly Arg Lys Cys  
 35 40 45

Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly Glu Ser  
 50 55 60

Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn Ile Gly  
 65 70 75 80

Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr  
 85 90

&lt;210&gt; 202

&lt;211&gt; 47

&lt;212&gt; PRT

<213> *Conus radiatus*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(47)

<223> Xaa at residues 17 and 22 is Glu or gamma-carboxy-Glu; Xaa at  
 residues 13, 31, 46 and 47 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-  
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 202

Lys Cys Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Xaa Asn Cys Gly  
 1 5 10 15

Xaa Ser Cys Ser Cys Xaa Gly Leu His Ser Cys Arg Cys Thr Xaa Asn  
 20 25 30

Ile Gly Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Xaa Xaa  
 35 40 45

&lt;210&gt; 203

&lt;211&gt; 338

&lt;212&gt; DNA

<213> *Conus radiatus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(264)

&lt;400&gt; 203

atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttc acc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
 1 5 10 15

ctg gca tcc agg cag cag gaa gga gat gtc cag gca agg aaa aca cgc 96  
 Leu Ala Ser Arg Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg  
 20 25 30

ctg acg agc gac ttc tat agt gtt ctg caa agg tat gga cta gga tgc 144

Leu	Thr	Ser	Asp	Phe	Tyr	Ser	Val	Leu	Gln	Arg	Tyr	Gly	Leu	Gly	Cys	
		35					40					45				
gct	ggc	act	tgt	ggc	tca	agc	agc	aat	tgt	gtt	aga	gat	tat	tgt	gac	192
Ala	Gly	Thr	Cys	Gly	Ser	Ser	Ser	Asn	Cys	Val	Arg	Asp	Tyr	Cys	Asp	
	50					55				60						
tgc	cca	aaa	ccc	aat	tgt	tac	tgc	act	ggc	aaa	ggc	ttt	cgt	caa	cca	240
Cys	Pro	Lys	Pro	Asn	Cys	Tyr	Cys	Thr	Gly	Lys	Gly	Phe	Arg	Gln	Pro	
65					70					75					80	
gga	tgc	ggg	tgt	tca	tgt	ttg	ggg	tgattaattg	gctcttttaa	ctcgttgaac						294
Gly	Cys	Gly	Cys	Ser	Cys	Leu	Gly									
				85												
gatttaaaaa atccagagca atatgttcga gaaaaaccga agac																338

<210>	204
<211>	88
<212>	PRT
<213>	Conus radiatus

<400>	204
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr	
1	5 10 15
Leu Ala Ser Arg Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg	
	20 25 30
Leu Thr Ser Asp Phe Tyr Ser Val Leu Gln Arg Tyr Gly Leu Gly Cys	
	35 40 45
Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val Arg Asp Tyr Cys Asp	
	50 55 60
Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys Gly Phe Arg Gln Pro	
65	70 75 80
Gly Cys Gly Cys Ser Cys Leu Gly	
	85

<210>	205
<211>	44
<212>	PRT
<213>	Conus radiatus

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<220>
<221> PEPTIDE
<222> (1)..(44)
<223> Xaa at residues 23, 25 and 37 is Pro or hydroxy-Pro; Xaa at
      residues 1, 19 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
      iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

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<400> 205
Xaa Gly Leu Gly Cys Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val
1          5          10
Arg Asp Xaa Cys Asp Cys Xaa Lys Xaa Asn Cys Xaa Cys Thr Gly Lys
          20          25          30

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Gly Phe Arg Gln Xaa Gly Cys Gly Cys Ser Cys Leu  
           35                                  40

<210> 206  
 <211> 375  
 <212> DNA  
 <213> Conus sponsalis

<220>  
 <221> CDS  
 <222> (24)..(260)

<400> 206  
 gacaggattg aacaaaattc agg atg tca gga ttg gga atc atg gtg ctg acc 53  
                                   Met Ser Gly Leu Gly Ile Met Val Leu Thr  
                                   1                                  5                                  10

ctt ttg ctt ctt gtg tcc atg gca acc agc cat aag gat gga gga gag 101  
 Leu Leu Leu Leu Val Ser Met Ala Thr Ser His Lys Asp Gly Gly Glu  
                                   15                                  20                                  25

aag cag gcg atg caa agg gac gca atc aac gtc aga ctg aga aga tca 149  
 Lys Gln Ala Met Gln Arg Asp Ala Ile Asn Val Arg Leu Arg Arg Ser  
                                   30                                  35                                  40

ctc act cgg aga gca gta act gag gcg tgc acg gag gac tgt aag act 197  
 Leu Thr Arg Arg Ala Val Thr Glu Ala Cys Thr Glu Asp Cys Lys Thr  
                                   45                                  50                                  55

cag gac aag aag tgc tgc ggc gaa atg aat gga caa cac aca tgt gcc 245  
 Gln Asp Lys Lys Cys Cys Gly Glu Met Asn Gly Gln His Thr Cys Ala  
                                   60                                  65                                  70

aag ata tgc ctc gga tagtctctgt acgctgtctc attcattatc tcatcagtac 300  
 Lys Ile Cys Leu Gly  
 75

aagtgtaaac gagacaggtc agaaagtcga aggttggttcg aaatttgata agcattgttt 360

actgggacga acgga 375

<210> 207  
 <211> 79  
 <212> PRT  
 <213> Conus sponsalis

<400> 207  
 Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser  
 1                                  5                                  10                                  15

Met Ala Thr Ser His Lys Asp Gly Gly Glu Lys Gln Ala Met Gln Arg  
                                   20                                  25                                  30

Asp Ala Ile Asn Val Arg Leu Arg Arg Ser Leu Thr Arg Arg Ala Val  
                                   35                                  40                                  45

Thr Glu Ala Cys Thr Glu Asp Cys Lys Thr Gln Asp Lys Lys Cys Cys  
                                   50                                  55                                  60

Gly Glu Met Asn Gly Gln His Thr Cys Ala Lys Ile Cys Leu Gly

65

70

75

&lt;210&gt; 208

&lt;211&gt; 32

&lt;212&gt; PRT

<213> *Conus sponsalis*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(32)

&lt;223&gt; Xaa at residues 4, 8 and 20 is Glu or gamma-carboxy-Glu

&lt;400&gt; 208

Ala	Val	Thr	Xaa	Ala	Cys	Thr	Xaa	Asp	Cys	Lys	Thr	Gln	Asp	Lys	Lys
1				5				10					15		

Cys	Cys	Gly	Xaa	Met	Asn	Gly	Gln	His	Thr	Cys	Ala	Lys	Ile	Cys	Leu
		20					25						30		

&lt;210&gt; 209

&lt;211&gt; 8

&lt;212&gt; PRT

<213> *Conus stercusmuscarum*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(8)

&lt;223&gt; Xaa at residues 3 and 6 is Pro or hydroxy-Pro; Xaa at residue 4 is D-Trp

&lt;400&gt; 209

Gly	Cys	Xaa	Xaa	Gln	Xaa	Val	Cys
1			5				

&lt;210&gt; 210

&lt;211&gt; 9

&lt;212&gt; PRT

<213> *Conus striatus*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(9)

&lt;223&gt; Xaa at residue 7 is Pro or hydroxy-Pro

&lt;400&gt; 210

Cys	Ile	Ile	Arg	Asn	Cys	Xaa	Arg	Gly
1				5				

&lt;210&gt; 211

&lt;211&gt; 238

&lt;212&gt; DNA

<213> *Conus striatus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(96)

&lt;400&gt; 211

agg	tcg	act	cgc	tgc	ttg	cct	gac	gga	acg	tct	tgc	ctt	ttt	agt	agg
Ser	Thr	Arg	Cys	Leu	Pro	Asp	Gly	Thr	Ser	Cys	Leu	Phe	Ser	Arg	

1	5	10	15	
atc aga tgc tgc ggt act tgc agt tca atc tta aag tca tgt gtg agc				96
Ile Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser				
	20	25	30	
tgatccagcg gttgatcttc ctccctctgt gctccatcct tttctgcctg agttctcctt				156
acctgagagt ggtcatgaac cactcatcac ctactcttct ggaggcttca gaggagctac				216
agtgaataa aagccgcatt gc				238
<210> 212				
<211> 31				
<212> PRT				
<213> Conus striatus				
<400> 212				
Ser Thr Arg Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile				
1	5	10	15	
Arg Cys Cys Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser				
	20	25	30	
<210> 213				
<211> 28				
<212> PRT				
<213> Conus striatus				
<220>				
<221> PEPTIDE				
<222> (1)..(28)				
<223> Xaa at residue 3 is Pro or hydroxy-Pro				
<400> 213				
Cys Leu Xaa Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys				
1	5	10	15	
Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser				
	20	25		
<210> 214				
<211> 707				
<212> DNA				
<213> Conus striatus				
<220>				
<221> CDS				
<222> (171)..(539)				
<400> 214				
cggcttctaa tacgactcac tatagggcaa gcagtggtaa caacgcagag tacgcggggg				60
gacggcagac cagctgggga ccagacagac gtcaaacagc atcgcagtca ggtgtggaga				120
tccaagaca cccagaagaa ggagacagaa gagttatcgt tcgtaacaca atg gcc				176
			Met Ala	
			1	
atg aac atg tcg atg aca ctc tgc atg ttt gta atg gtc gtc gtg gca				224

Met	Asn	Met	Ser	Met	Thr	Leu	Cys	Met	Phe	Val	Met	Val	Val	Val	Ala		
	5						10					15					
gcc	act	gtc	att	gat	tcc	act	cag	tta	caa	gaa	cca	gat	ctc	agt	cgc	272	
Ala	Thr	Val	Ile	Asp	Ser	Thr	Gln	Leu	Gln	Glu	Pro	Asp	Leu	Ser	Arg		
	20					25				30							
atg	cga	cgc	agc	ggg	cct	gct	gac	tgt	tgc	agg	atg	aaa	gag	tgt	tgc	320	
Met	Arg	Arg	Ser	Gly	Pro	Ala	Asp	Cys	Cys	Arg	Met	Lys	Glu	Cys	Cys		
	35			40				45						50			
acc	gac	aga	gtg	aac	gag	tgt	cta	cag	cgc	tat	tct	ggc	cgg	gaa	gat	368	
Thr	Asp	Arg	Val	Asn	Glu	Cys	Leu	Gln	Arg	Tyr	Ser	Gly	Arg	Glu	Asp		
				55				60					65				
aaa	ttc	gtt	tcg	ttt	tgt	tat	cag	gag	gcc	aca	gtc	aca	tgt	gga	tct	416	
Lys	Phe	Val	Ser	Phe	Cys	Tyr	Gln	Glu	Ala	Thr	Val	Thr	Cys	Gly	Ser		
		70					75						80				
ttt	aac	gaa	atc	gtg	ggc	tgt	tgc	tat	gga	tat	caa	atg	tgc	atg	ata	464	
Phe	Asn	Glu	Ile	Val	Gly	Cys	Cys	Tyr	Gly	Tyr	Gln	Met	Cys	Met	Ile		
	85					90					95						
cga	gtt	gtg	aaa	ccg	aac	agt	cta	agt	ggg	gcc	cat	gag	gcg	tgc	aaa	512	
Arg	Val	Val	Lys	Pro	Asn	Ser	Leu	Ser	Gly	Ala	His	Glu	Ala	Cys	Lys		
	100				105				110								
acc	gtt	tct	tgt	ggc	aac	cct	tgc	gct	tgagg	gtgcc	tcgcg	ccacg				559	
Thr	Val	Ser	Cys	Gly	Asn	Pro	Cys	Ala									
	115				120												
tcacctgtgt acagcgccgt caccagagcc ctgatcttta tgcccttata tgtctttttg																	619
ctctttcact ctctgaagtc ttgagggttg ttccattctt gtcaatcatc tcacgcgcat																	679
ccaagtaaat aaaggtgacg tgacaaac																	707
<210> 215																	
<211> 123																	
<212> PRT																	
<213> Conus striatus																	
<400> 215																	
Met	Ala	Met	Asn	Met	Ser	Met	Thr	Leu	Cys	Met	Phe	Val	Met	Val	Val		
1			5					10					15				
Val	Ala	Ala	Thr	Val	Ile	Asp	Ser	Thr	Gln	Leu	Gln	Glu	Pro	Asp	Leu		
			20				25					30					
Ser	Arg	Met	Arg	Arg	Ser	Gly	Pro	Ala	Asp	Cys	Cys	Arg	Met	Lys	Glu		
	35					40					45						
Cys	Cys	Thr	Asp	Arg	Val	Asn	Glu	Cys	Leu	Gln	Arg	Tyr	Ser	Gly	Arg		
	50				55					60							
Glu	Asp	Lys	Phe	Val	Ser	Phe	Cys	Tyr	Gln	Glu	Ala	Thr	Val	Thr	Cys		
	65			70				75						80			
Gly	Ser	Phe	Asn	Glu	Ile	Val	Gly	Cys	Cys	Tyr	Gly	Tyr	Gln	Met	Cys		
			85					90					95				

Met Ile Arg Val Val Lys Pro Asn Ser Leu Ser Gly Ala His Glu Ala  
                   100                  105                  110

Cys Lys Thr Val Ser Cys Gly Asn Pro Cys Ala  
           115                  120

<210> 216

<211> 86

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(86)

<223> Xaa at residues 11, 19, 28, 38, 48 and 74 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 66 and 84 is Pro or hydroxy-Pro; Xaa at residues 24, 26, 54 and 56 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 216

Ser Gly Xaa Ala Asp Cys Cys Arg Met Lys Xaa Cys Cys Thr Asp Arg  
 1                  5                  10                  15

Val Asn Xaa Cys Leu Gln Arg Xaa Ser Gly Arg Xaa Asp Lys Phe Val  
           20                  25                  30

Ser Phe Cys Xaa Gln Xaa Ala Thr Val Thr Cys Gly Ser Phe Asn Xaa  
           35                  40                  45

Ile Val Gly Cys Cys Xaa Gly Xaa Gln Met Cys Met Ile Arg Val Val  
       50                  55                  60

Lys Xaa Asn Ser Leu Ser Gly Ala His Xaa Ala Cys Lys Thr Val Ser  
 65                  70                  75                  80

Cys Gly Asn Xaa Cys Ala  
                   85

<210> 217

<211> 14

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residues 1 and 3 is Trp (D or L) or bromo-Trp (D or L)

<400> 217

Xaa Ser Xaa Arg Met Gly Asn Gly Asp Arg Arg Ser Asp Gln  
 1                  5                  10

<210> 218

<211> 343

<212> DNA

<213> Conus striolatus

<220>

<221> CDS

<222> (1)..(276)

<400> 218  
 atg atg tcg aaa atg gga gct atg ttt gtc ctt ttg ctt ctt ttg acc 48  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Leu Thr  
 1 5 10 15  
  
 ctg gca tcc agc cag cag gag gga gat gtc cag gca agg aaa aca agc 96  
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser  
 20 25 30  
  
 ctg aag agc gac ttc tat cgt gct ctg aga ccg tat gac aga cag tgc 144  
 Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Pro Tyr Asp Arg Gln Cys  
 35 40 45  
  
 act ttt gtc aac aat tgt caa cag aac ggt gcg tgt aac ggt gat tgc 192  
 Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly Asp Cys  
 50 55 60  
  
 tct tgc ggg gac cag att tgt aaa tgc ggt tat aga atc agt cct ggg 240  
 Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser Pro Gly  
 65 70 75 80  
  
 agg tca gga tgc gcg tgt act tgt aga aat gcc aaa tgaatcactt 286  
 Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
 85 90  
  
 aactcgttga aagattttta aaaatccaga gctatatgtt cgagaaaaac cgaagac 343  
  
 <210> 219  
 <211> 92  
 <212> PRT  
 <213> *Conus striolatus*  
  
 <400> 219  
 Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Leu Thr  
 1 5 10 15  
  
 Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Ser  
 20 25 30  
  
 Leu Lys Ser Asp Phe Tyr Arg Ala Leu Arg Pro Tyr Asp Arg Gln Cys  
 35 40 45  
  
 Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly Asp Cys  
 50 55 60  
  
 Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser Pro Gly  
 65 70 75 80  
  
 Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
 85 90  
  
 <210> 220  
 <211> 46  
 <212> PRT  
 <213> *Conus striolatus*  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(46)



<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 33 is Pro or hydroxy-Pro; Xaa at residue 29 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 220

Xaa Cys Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Ala Cys Asn Gly  
1 5 10 15

Asp Cys Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Xaa Arg Ile Ser  
20 25 30

Xaa Gly Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
35 40 45

<210> 221

<211> 398

<212> DNA

<213> Conus tessulatus

<220>

<221> CDS

<222> (7)..(240)

<400> 221

ggatcc atg aaa ctg acg tgt gtg gtg atc atc gcc gtg ctg ttc ctg 48  
Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu  
1 5 10

acg gcc tgt caa ttc att ata gct gat ttc tcc aga gat aag cgg gta 96  
Thr Ala Cys Gln Phe Ile Ile Ala Asp Phe Ser Arg Asp Lys Arg Val  
15 20 25 30

cat cgt gca gag agg ttg aga gac ata atg cag aat ttc aga ggt acc 144  
His Arg Ala Glu Arg Leu Arg Asp Ile Met Gln Asn Phe Arg Gly Thr  
35 40 45

agg tcg tgc gcg gaa ttt ggt gaa gtt tgt agt tct acc gct tgc tgc 192  
Arg Ser Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys  
50 55 60

cct gat ttg gat tgc gtt gag gcc tat tca ccc atc tgt ctc tgg gaa 240  
Pro Asp Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu  
65 70 75

tagtctggca tctgatattt cccgtctgtg ctctacctac ttctgccgga ttcattcata 300

cctatgtgtg gccatgaacc actcagtacc tacacctctg gtggcttcct agggacgtat 360

atcaaaataa aaccacattg caaaaaaaaaa aaaaaaaaaa 398

<210> 222

<211> 78

<212> PRT

<213> Conus tessulatus

<400> 222

Met Lys Leu Thr Cys Val Val Ile Ile Ala Val Leu Phe Leu Thr Ala  
1 5 10 15

Cys Gln Phe Ile Ile Ala Asp Phe Ser Arg Asp Lys Arg Val His Arg

20 25 30

Ala Glu Arg Leu Arg Asp Ile Met Gln Asn Phe Arg Gly Thr Arg Ser  
35 40 45

Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys Pro Asp  
50 55 60

Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu  
65 70 75

<210> 223  
<211> 31  
<212> PRT  
<213> Conus tessulatus

<220>  
<221> PEPTIDE  
<222> (1)..(31)  
<223> Xaa at residues 4, 7 and 22 is Glu or gamma-carboxy-Glu; Xaa at residues 16 and 26 is Pro or hydroxy-Pro; Xaa at residue 30 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 24 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 223  
Ser Cys Ala Xaa Phe Gly Xaa Val Cys Ser Ser Thr Ala Cys Cys Xaa  
1 5 10 15

Asp Leu Asp Cys Val Xaa Ala Xaa Ser Xaa Ile Cys Leu Xaa Xaa  
20 25 30

<210> 224  
<211> 273  
<212> DNA  
<213> Conus textile

<400> 224  
cgattgcagg ggttacgatg cgccgtgtag ctctggcgcg ccatgttggtg attggtggac 60  
atgttcagca cgaaccaacc gctgttttta ggctgaccac aagccatccg acatcaccac 120  
tctcctcttc agaggcttca aggcctttttg ttctcctttt gaagaatctt tacgagttaa 180  
caaacaagta gaatagcacg tttttccccc ttgaaaaat caataatgga ggtaaataa 240  
aactgtcttc ttcaataaag attttatcat aat 273

<210> 225  
<211> 50  
<212> PRT  
<213> Conus textile

<400> 225  
Ile Gln Gly Gly Gly Asp Glu Arg Gln Lys Ala Lys Ile Asn Phe Leu  
1 5 10 15

Ser Arg Ser Asp Arg Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser  
20 25 30

Gly Ala Pro Cys Cys Asp Trp Trp Thr Cys Ser Ala Arg Thr Asn Arg

	35	40	45	
Cys Phe				
50				
<210>	226			
<211>	29			
<212>	PRT			
<213>	Conus textile			
<220>				
<221>	PEPTIDE			
<222>	(1)..(29)			
<223>	Xaa at residues 8 and 14 is Pro or hydroxy-Pro; Xaa at residues 18 and 19 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr			
<400>	226			
Asp Cys Arg Gly Xaa Asp Ala Xaa Cys Ser Ser Gly Ala Xaa Cys Cys				
1	5	10	15	
Asp Xaa Xaa Thr Cys Ser Ala Arg Thr Asn Arg Cys Phe				
	20	25		
<210>	227			
<211>	23			
<212>	PRT			
<213>	Conus textile			
<220>				
<221>	PEPTIDE			
<222>	(1)..(23)			
<223>	Xaa at residue 16 is Glu or gamma-carboxy-Glu; Xaa at residues 3, 11, 12, 22 and 23 is Pro or hydroxy-Pro; Xaa at residues 4, 5 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr			
<400>	227			
Asn Cys Xaa Xaa Cys Val Val Xaa Cys Cys Xaa Xaa Ala Xaa Cys Xaa				
1	5	10	15	
Ala Ser Gly Cys Arg Xaa Xaa				
	20			
<210>	228			
<211>	205			
<212>	DNA			
<213>	Conus textile			
<220>				
<221>	CDS			
<222>	(1)..(186)			
<400>	228			
atg cac tgt ctc cca atc ttc gtc att ctt ctg ctg ctg act gca tct				48
Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser				
1	5	10	15	
gga cct agc gtt gat gcc caa ctg aag acc aaa gat gat gtg ccc ctg				96

Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu  
                   20                  25                  30

tca tct ttc cga gat cat gca aag agt acc cta cga aga ctt cag gac      144  
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp  
           35                  40                  45

aaa cag act tgc tgt ggc tat agg atg tgt gtt cct tgt ggt      186  
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly  
       50                  55                  60

taaccagcat gaaggatcc      205

<210> 229  
 <211> 62  
 <212> PRT  
 <213> Conus textile

<400> 229  
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1                  5                  10                  15

Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu  
                   20                  25                  30

Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp  
           35                  40                  45

Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly  
       50                  55                  60

<210> 230  
 <211> 12  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or  
       hydroxy-Pro; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr,  
       di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 230  
 Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys  
 1                  5                  10

<210> 231  
 <211> 115  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (2)..(94)

<400> 231  
 g tta tgg agc gat tgc tat agt tgg tta gga tca tgt att gcg ccc tcg      49  
   Leu Trp Ser Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser  
    1                  5                  10                  15

cag tgt tgt tct gag gtt tgt gat tat tac tgc cgc cta tgg cga 94  
 Gln Cys Cys Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg  
                   20                  25                  30

tgaactcgga ccacaagcca t 115

<210> 232  
 <211> 31  
 <212> PRT  
 <213> Conus textile

<400> 232  
 Leu Trp Ser Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser  
 1                  5                  10                  15

Gln Cys Cys Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg  
                   20                  25                  30

<210> 233  
 <211> 28  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(28)  
 <223> Xaa at residue 18 is Glu or gamma-carboxy-Glu; Xaa at residue 13  
       is Pro or hydroxy-Pro; Xaa at residues 5 and 27 is Trp (D or L)  
       or bromo-Trp (D or L); Xaa at residue 3, 22 and 23 is Tyr, 125I-Tyr  
       , mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 233  
 Asp Cys Xaa Ser Xaa Leu Gly Ser Cys Ile Ala Xaa Ser Gln Cys Cys  
 1                  5                  10                  15

Ser Xaa Val Cys Asp Xaa Xaa Cys Arg Leu Xaa Arg  
                   20                  25

<210> 234  
 <211> 279  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (7)..(126)

<400> 234  
 agctga cga atg aaa aat tcc gag aat gtc aag ctc agc aag aga aaa 48  
       Arg Met Lys Asn Ser Glu Asn Val Lys Leu Ser Lys Arg Lys  
       1                  5                  10

tgt gtg gaa caa tgg aaa tac tgc acc cga gag tcc tta tgt tgc gcg 96  
 Cys Val Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys Ala  
 15                  20                  25                  30

ggt ttg tgt ttg ttt agt ttc tgc att cta taacgcta ctagagtcgt 146  
 Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu  
                   35                  40

atattccgtc taagctccac ctggcactgt ctggtatggt cctgccagtg actggtctca 206  
 taccgcttag actctgggtcc gtcttctctg caaccacagg agaacgtgca ttattacaat 266  
 aaacgcatac tgc 279

<210> 235  
 <211> 40  
 <212> PRT  
 <213> Conus textile

<400> 235  
 Arg Met Lys Asn Ser Glu Asn Val Lys Leu Ser Lys Arg Lys Cys Val  
 1 5 10 15  
 Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys Ala Gly Leu  
 20 25 30  
 Cys Leu Phe Ser Phe Cys Ile Leu  
 35 40

<210> 236  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 4 and 12 is Glu or gamma-carboxy-Glu; Xaa at  
 residue 6 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 8  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 236  
 Lys Cys Val Xaa Gln Xaa Lys Xaa Cys Thr Arg Xaa Ser Leu Cys Cys  
 1 5 10 15  
 Ala Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu  
 20 25

<210> 237  
 <211> 510  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (223)..(471)

<400> 237  
 cagagccgct ctggtgtgca gacctgtctc cagccctccg tctccctgat cggtggttct 60  
 gctgcatag ctgtcttctc cacgaagctt tccacaggta taaataacgc ttcagtctcc 120  
 cgtcctgtat tgggccgccg ttacaagcca gaccgatata gccaggcca gtctactttg 180  
 cgagtgagtt aaaagctcca gcattctacc agcatcacca ga atg aag gtg agc 234  
 Met Lys Val Ser

1

agc gtg ctg atc gtg gct acg ctg aca ctg acc gca ggc cag ctg gtt 282  
 Ser Val Leu Ile Val Ala Thr Leu Thr Leu Thr Ala Gly Gln Leu Val  
 5 10 15 20

agt gct tct tcc cat tac tca aaa gat gtc cag att ctt cct tct gtg 330  
 Ser Ala Ser Ser His Tyr Ser Lys Asp Val Gln Ile Leu Pro Ser Val  
 25 30 35

aga tca gct gac gaa gtg gaa aat tcc gag aat gtc agg ctc agc aag 378  
 Arg Ser Ala Asp Glu Val Glu Asn Ser Glu Asn Val Arg Leu Ser Lys  
 40 45 50

aga aga tgt gtg gaa caa tgg gaa gtc tgc ggc ata atc ttg ttc tcc 426  
 Arg Arg Cys Val Glu Gln Trp Glu Val Cys Gly Ile Ile Leu Phe Ser  
 55 60 65

tca tca tgt tgc ggg cag ttg tgt ttg ttt ggt ttc tgc gtt cta 471  
 Ser Ser Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu  
 70 75 80

taacgctaata ccagagtcgt atattccgtc taagctcca 510

<210> 238  
 <211> 83  
 <212> PRT  
 <213> Conus textile

<400> 238  
 Met Lys Val Ser Ser Val Leu Ile Val Ala Thr Leu Thr Leu Thr Ala  
 1 5 10 15

Gly Gln Leu Val Ser Ala Ser Ser His Tyr Ser Lys Asp Val Gln Ile  
 20 25 30

Leu Pro Ser Val Arg Ser Ala Asp Glu Val Glu Asn Ser Glu Asn Val  
 35 40 45

Arg Leu Ser Lys Arg Arg Cys Val Glu Gln Trp Glu Val Cys Gly Ile  
 50 55 60

Ile Leu Phe Ser Ser Ser Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe  
 65 70 75 80

Cys Val Leu

<210> 239  
 <211> 29  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residues 3 and 6 is Glu or gamma-carboxy-Glu; Xaa at  
 residue 5 is Trp (D or L) or bromo-Trp (D or L)

<400> 239  
 Cys Val Xaa Gln Xaa Xaa Val Cys Gly Ile Ile Leu Phe Ser Ser Ser





aag cag gcg acg cga agg gac gca gtc aac gtc aga cgg aga agc aga 147  
 Lys Gln Ala Thr Arg Arg Asp Ala Val Asn Val Arg Arg Arg Ser Arg  
                   30                                  35                                  40

cca aaa aca aag gag tgc gaa agg tac tgt gag ctg gag gaa aag cac 195  
 Pro Lys Thr Lys Glu Cys Glu Arg Tyr Cys Glu Leu Glu Glu Lys His  
                   45                                  50                                  55

tgc tgc tgc ata aga agt aac gga ccc aaa tgt tcc aga ata tgc ata 243  
 Cys Cys Cys Ile Arg Ser Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile  
                   60                                  65                                  70

ttc aaa ttt tgg tgt tagttttctg tacactgtcc attcattatc ttatcagtac 298  
 Phe Lys Phe Trp Cys  
 75

aagtgtaaac gagacatgtc agaaagtcga aggttgtgcg taatttgata agcattgttt 358

actgggacga acgga 373

<210> 243

<211> 79

<212> PRT

<213> Conus tulipa

<400> 243

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Ser  
 1                                  5                                  10                                  15

Met Ala Thr Ser His Arg Tyr Ala Arg Glu Lys Gln Ala Thr Arg Arg  
                   20                                  25                                  30

Asp Ala Val Asn Val Arg Arg Arg Ser Arg Pro Lys Thr Lys Glu Cys  
                   35                                  40                                  45

Glu Arg Tyr Cys Glu Leu Glu Glu Lys His Cys Cys Cys Ile Arg Ser  
                   50                                  55                                  60

Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile Phe Lys Phe Trp Cys  
 65                                  70                                  75

<210> 244

<211> 37

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 5, 7, 11, 13 and 14 is Glu or gamma-carboxy-Glu;  
 Xaa at residues 1 and 25 is Pro or hydroxy-Pro; Xaa at residue 36  
 is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr

<400> 244

Xaa Lys Thr Lys Xaa Cys Xaa Arg Xaa Cys Xaa Leu Xaa Xaa Lys His  
1 5 10 15

Cys Cys Cys Ile Arg Ser Asn Gly Xaa Lys Cys Ser Arg Ile Cys Ile  
20 25 30

Phe Lys Phe Xaa Cys  
35

<210> 245

<211> 381

<212> DNA

<213> Conus tulipa

<220>

<221> CDS

<222> (22)..(267)

<400> 245

caggattgaa caaaattcag g atg tca gga ttg gga atc atg gtg cta acc 51  
Met Ser Gly Leu Gly Ile Met Val Leu Thr  
1 5 10

ctt ctc ctt ctt gtg cta atg aca acc agt cat cag gat gca gga gag 99  
Leu Leu Leu Leu Val Leu Met Thr Thr Ser His Gln Asp Ala Gly Glu  
15 20 25

aag cag gcg atg caa agg gac gca aag aac ttc agt cgg aga aga tta 147  
Lys Gln Ala Met Gln Arg Asp Ala Lys Asn Phe Ser Arg Arg Arg Leu  
30 35 40

gtc att cgg aga cca aaa aca agg gag tgc gaa atg cag tgt gag cag 195  
Val Ile Arg Arg Pro Lys Thr Arg Glu Cys Glu Met Gln Cys Glu Gln  
45 50 55

gag gag aaa cac tgc tgc cgc gta aga gat ggt acg ggc caa tgt gcc 243  
Glu Glu Lys His Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala  
60 65 70

cct aag tgc ttg gga att aac tgg tagtttctgt acactgtctc attcattatc 297  
Pro Lys Cys Leu Gly Ile Asn Trp  
75 80

ttatcagttac acgtgtaacg agacatgtca gaaagtcgaa ggtagtgcgt aatttgataa 357

gcattgttta ctgggacgaa cgga 381

<210> 246

<211> 82

<212> PRT

<213> Conus tulipa

<400> 246

Met Ser Gly Leu Gly Ile Met Val Leu Thr Leu Leu Leu Leu Val Leu  
1 5 10 15

Met Thr Thr Ser His Gln Asp Ala Gly Glu Lys Gln Ala Met Gln Arg  
20 25 30

Asp Ala Lys Asn Phe Ser Arg Arg Arg Leu Val Ile Arg Arg Pro Lys

		35						40						45					
Thr	Arg	Glu	Cys	Glu	Met	Gln	Cys	Glu	Gln	Glu	Glu	Lys	His	Cys	Cys				
	50					55					60								

Arg	Val	Arg	Asp	Gly	Thr	Gly	Gln	Cys	Ala	Pro	Lys	Cys	Leu	Gly	Ile				
65					70					75					80				

Asn Trp

<210> 247

<211> 36

<212> PRT

<213> Conus tulipa

<220>

<221> PEPTIDE

<222> (1)..(36)

<223> Xaa at residues 5, 7, 11, 13 and 14 is Glu or gamma-carboxy-Glu;  
Xaa at residues 1 and 29 is Pro or hydroxy-Pro; Xaa at residue 36  
is Trp (D or L) or bromo-Trp (D or L)

<400> 247

Xaa	Lys	Thr	Arg	Xaa	Cys	Xaa	Met	Gln	Cys	Xaa	Gln	Xaa	Xaa	Lys	His				
1				5				10						15					

Cys	Cys	Arg	Val	Arg	Asp	Gly	Thr	Gly	Gln	Cys	Ala	Xaa	Lys	Cys	Leu				
		20						25					30						

Gly	Ile	Asn	Xaa																
		35																	

<210> 248

<211> 363

<212> DNA

<213> Conus tulipa

<220>

<221> CDS

<222> (1)..(264)

<400> 248

atg	atg	tcg	aaa	atg	gga	gct	atg	ttt	gtc	ctt	ttg	ctt	ctt	ttc	acc				48
Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Thr				
1				5				10						15					

ctg	gca	tcc	agc	cag	cag	gaa	gga	gat	gtc	cag	gca	agg	aaa	aca	cgc				96
Leu	Ala	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	Arg				
		20						25					30						

ctg	aag	agc	gac	ttc	tat	cgt	gct	ctg	cca	agg	ttt	ggc	cca	ata	tgc				144
Leu	Lys	Ser	Asp	Phe	Tyr	Arg	Ala	Leu	Pro	Arg	Phe	Gly	Pro	Ile	Cys				
		35					40					45							

act	tgt	ttt	aaa	agc	cag	aac	tgt	cgg	ggt	tct	tgt	gaa	tgc	atg	tca				192
Thr	Cys	Phe	Lys	Ser	Gln	Asn	Cys	Arg	Gly	Ser	Cys	Glu	Cys	Met	Ser				
	50					55					60								

cct	ccc	ggt	tgt	tac	tgc	agt	aac	aat	ggc	att	cgt	gaa	cga	gga	tgc				240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--	--	-----

Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile Arg Glu Arg Gly Cys  
65 70 75 80

tcg tgt aca tgt cca ggg act ggt tgaatgattt gaaaaattca gagcaatatg 294  
Ser Cys Thr Cys Pro Gly Thr Gly  
85

ttgcagaaaa accgaagacc gagacttctc acaataaatc cataaagaca ttaaaaaaaaa 354  
aaaaaaaaa 363

<210> 249  
<211> 88  
<212> PRT  
<213> Conus tulipa

<400> 249  
Met Met Ser Lys Met Gly Ala Met Phe Val Leu Leu Leu Leu Phe Thr  
1 5 10 15

Leu Ala Ser Ser Gln Gln Glu Gly Asp Val Gln Ala Arg Lys Thr Arg  
20 25 30

Leu Lys Ser Asp Phe Tyr Arg Ala Leu Pro Arg Phe Gly Pro Ile Cys  
35 40 45

Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser Cys Glu Cys Met Ser  
50 55 60

Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile Arg Glu Arg Gly Cys  
65 70 75 80

Ser Cys Thr Cys Pro Gly Thr Gly  
85

<210> 250  
<211> 44  
<212> PRT  
<213> Conus tulipa

<220>  
<221> PEPTIDE  
<222> (1)..(44)  
<223> Xaa at residues 18 and 34 is Glu or gamma-carboxy-Glu; Xaa at  
residues 3, 22, 23 and 42 is Pro or hydroxy-Pro; Xaa at residue 26  
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Tyr

<400> 250  
Phe Gly Xaa Ile Cys Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser  
1 5 10 15

Cys Xaa Cys Met Ser Xaa Xaa Gly Cys Xaa Cys Ser Asn Asn Gly Ile  
20 25 30

Arg Xaa Arg Gly Cys Ser Cys Thr Cys Xaa Gly Thr  
35 40

<210> 251  
<211> 383

&lt;212&gt; DNA

&lt;213&gt; Conus tulipa

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(276)

&lt;400&gt; 251

atg	atg	tcg	aaa	atg	gga	gct	atg	ttt	gtc	ctt	ttg	ctt	ctt	ttc	acc	48
Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Thr	
1				5					10					15		

ctg	gca	tcc	agc	cag	cag	gaa	gga	gat	gtc	cag	gca	agg	aaa	aca	cgc	96
Leu	Ala	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	Arg	
			20					25					30			

ctg	aag	agc	gac	ttc	tat	cgt	act	ctg	gca	ata	tct	gac	aga	gga	tgc	144
Leu	Lys	Ser	Asp	Phe	Tyr	Arg	Thr	Leu	Ala	Ile	Ser	Asp	Arg	Gly	Cys	
		35					40					45				

act	ggc	aac	tgt	gat	tgg	acg	tgt	agc	ggg	gat	tgc	agc	tgc	cag	ggc	192
Thr	Gly	Asn	Cys	Asp	Trp	Thr	Cys	Ser	Gly	Asp	Cys	Ser	Cys	Gln	Gly	
	50					55				60						

aca	tct	gac	tcg	tgt	cac	tgc	att	cca	cca	aaa	tca	ata	ggc	aac	aga	240
Thr	Ser	Asp	Ser	Cys	His	Cys	Ile	Pro	Pro	Lys	Ser	Ile	Gly	Asn	Arg	
65					70					75					80	

tgc	cgg	tgt	cag	tgt	aaa	aga	aaa	atc	gaa	att	gac	tgattctttt				286
Cys	Arg	Cys	Gln	Cys	Lys	Arg	Lys	Ile	Glu	Ile	Asp					
				85					90							

aactcgttga	acgatttaaa	aatcagacca	atatgtaggc	agaaaaccga	agactctgag	346
------------	------------	------------	------------	------------	------------	-----

actctcgtaa	taatcgtaag	caaaaaaaaa	aaaaaaaa	383
------------	------------	------------	----------	-----

&lt;210&gt; 252

&lt;211&gt; 92

&lt;212&gt; PRT

&lt;213&gt; Conus tulipa

&lt;400&gt; 252

Met	Met	Ser	Lys	Met	Gly	Ala	Met	Phe	Val	Leu	Leu	Leu	Leu	Phe	Thr
1				5					10					15	

Leu	Ala	Ser	Ser	Gln	Gln	Glu	Gly	Asp	Val	Gln	Ala	Arg	Lys	Thr	Arg
			20					25					30		

Leu	Lys	Ser	Asp	Phe	Tyr	Arg	Thr	Leu	Ala	Ile	Ser	Asp	Arg	Gly	Cys
		35					40					45			

Thr	Gly	Asn	Cys	Asp	Trp	Thr	Cys	Ser	Gly	Asp	Cys	Ser	Cys	Gln	Gly
	50					55				60					

Thr	Ser	Asp	Ser	Cys	His	Cys	Ile	Pro	Pro	Lys	Ser	Ile	Gly	Asn	Arg
65					70					75					80

Cys	Arg	Cys	Gln	Cys	Lys	Arg	Lys	Ile	Glu	Ile	Asp				
				85					90						

<210> 253  
 <211> 46  
 <212> PRT  
 <213> Conus tulipa  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(46)  
 <223> Xaa at residue 44 is Glu or gamma-carboxy-Glu; Xaa at residues 27  
 and 28 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp (D or L)  
 or bromo-Trp (D or L)  
  
 <400> 253  
 Gly Cys Thr Gly Asn Cys Asp Xaa Thr Cys Ser Gly Asp Cys Ser Cys  
 1 5 10 15  
 Gln Gly Thr Ser Asp Ser Cys His Cys Ile Xaa Xaa Lys Ser Ile Gly  
 20 25 30  
 Asn Arg Cys Arg Cys Gln Cys Lys Arg Lys Ile Xaa Ile Asp  
 35 40 45  
  
 <210> 254  
 <211> 404  
 <212> DNA  
 <213> Conus virgo  
  
 <220>  
 <221> CDS  
 <222> (7)..(243)  
  
 <400> 254  
 ggatcc atg aaa ctg acg tgt gtg gtg atc atc act gtg ctg ttc ctg 48  
 Met Lys Leu Thr Cys Val Val Ile Ile Thr Val Leu Phe Leu  
 1 5 10  
  
 acg gcc agt cag ctc att aca gct gat tac tcc aga gat cag cgg cag 96  
 Thr Ala Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Gln Arg Gln  
 15 20 25 30  
  
 tac cgt gca gtg agg ttg gga gat gaa atg cgg aat ttc aaa ggt gcc 144  
 Tyr Arg Ala Val Arg Leu Gly Asp Glu Met Arg Asn Phe Lys Gly Ala  
 35 40 45  
 agg gac tgc ggg gga caa ggt gaa ggt tgt tat act caa cct tgc tgc 192  
 Arg Asp Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys  
 50 55 60  
  
 cct ggt ctg cgg tgc cgt ggc ggc ggt act gga gga ggc gta tgc cag 240  
 Pro Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln  
 65 70 75  
  
 ctg tagtaatagt ttggcatctg atatttcccc tctgtgctcc accctctttt 293  
 Leu  
  
 gcctgattca tccttaccta tgtgtggtca tgaaccactc agtagctaca cctctggtgg 353  
  
 attcagagaa cgtatatcaa aataaaaacca cattgcaata aaaaaaaaaa a 404  
  
 <210> 255

<211> 79  
 <212> PRT  
 <213> *Conus virgo*

<400> 255  
 Met Lys Leu Thr Cys Val Val Ile Ile Thr Val Leu Phe Leu Thr Ala  
 1 5 10 15  
 Ser Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Gln Arg Gln Tyr Arg  
 20 25 30  
 Ala Val Arg Leu Gly Asp Glu Met Arg Asn Phe Lys Gly Ala Arg Asp  
 35 40 45  
 Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys Pro Gly  
 50 55 60  
 Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu  
 65 70 75

<210> 256  
 <211> 32  
 <212> PRT  
 <213> *Conus virgo*

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residues 13  
 and 16 is Pro or hydroxy-Pro; Xaa at residue 10 is Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 256  
 Asp Cys Gly Gly Gln Gly Xaa Gly Cys Xaa Thr Gln Xaa Cys Cys Xaa  
 1 5 10 15  
 Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu  
 20 25 30

<210> 257  
 <211> 285  
 <212> DNA  
 <213> *Conus radiatus*

<220>  
 <221> CDS  
 <222> (4)..(225)

<400> 257  
 atc atg cag aaa ctg aca atc ctg ctt ctt gtt gct gct ata ctg atg 48  
 Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met  
 1 5 10 15  
 tcg acc cag gtc ctg att caa ggt ggt gga gaa aaa cgc caa aaa gtc 96  
 Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val  
 20 25 30  
 aac att ttt tca aaa aga aag aca gat gct gag acc tgg tgg gag ggc 144  
 Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly  
 35 40 45

gaa tgc tct aat tgg tta gga agt tgt tcg acg ccc tca aat tgc tgt 192  
 Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys  
           50                          55                          60

ctc aag agt tgt aat ggg cac tgc aca ttg tgg tgatgaactc tgaccacaaa 245  
 Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp  
           65                          70

gccatccaac atcaccgctc tcctcttcag agtcttcaag 285

<210> 258  
 <211> 74  
 <212> PRT  
 <213> Conus radiatus

<400> 258  
 Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met Ser  
 1                          5                          10                          15

Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val Asn  
           20                          25                          30

Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly Glu  
           35                          40                          45

Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys Leu  
           50                          55                          60

Lys Ser Cys Asn Gly His Cys Thr Leu Trp  
 65                          70

<210> 259  
 <211> 31  
 <212> PRT  
 <213> Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 3 and is Glu or gamma-carboxy-Glu; Xaa at residue  
       16 is Pro or hydroxy-Pro; Xaa at residues 1, 2, 9 and 31 is Trp  
       (D or L) or bromo-Trp (D or L)

<400> 259  
 Xaa Xaa Xaa Gly Xaa Cys Ser Asn Xaa Leu Gly Ser Cys Ser Thr Xaa  
 1                          5                          10                          15

Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Xaa  
           20                          25                          30

<210> 260  
 <211> 296  
 <212> DNA  
 <213> Conus radiatus

<220>  
 <221> CDS  
 <222> (1)..(237)



<400> 260  
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gta ctg atg 48  
 Ile Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met  
 1 5 10 15  
 tcc acc cag gcc ctg att caa ggt ggt gga gga aaa cgc caa cag gca 96  
 Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala  
 20 25 30  
 aag agc aag tat ttt tcc gaa aga aag gca cct gct aag cgt tgg ttt 144  
 Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe  
 35 40 45  
 gga cac gaa gaa tgc act tat tgg ttg ggg cct tgt gag gtg gac gac 192  
 Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp  
 50 55 60  
 acg tgt tgt tct gcc agt tgt gag tcc aag ttc tgc ggg ttg tgg 237  
 Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp  
 65 70 75  
 tgatggacac tgaccacaag tcatactaca tcgccactct cctgttcaga gtcttcaag 296  
 <210> 261  
 <211> 79  
 <212> PRT  
 <213> *Conus radiatus*

<400> 261  
 Ile Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met  
 1 5 10 15  
 Ser Thr Gln Ala Leu Ile Gln Gly Gly Gly Gly Lys Arg Gln Gln Ala  
 20 25 30  
 Lys Ser Lys Tyr Phe Ser Glu Arg Lys Ala Pro Ala Lys Arg Trp Phe  
 35 40 45  
 Gly His Glu Glu Cys Thr Tyr Trp Leu Gly Pro Cys Glu Val Asp Asp  
 50 55 60  
 Thr Cys Cys Ser Ala Ser Cys Glu Ser Lys Phe Cys Gly Leu Trp  
 65 70 75

<210> 262  
 <211> 33  
 <212> PRT  
 <213> *Conus radiatus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(33)  
 <223> Xaa at residues 5, 6, 15 and 26 is Glu or gamma-carboxy-Glu; Xaa  
 at residue 13 is Pro or hydroxy-Pro; Xaa at residues 1, 10 and 33  
 is Trp (D or L) or bromo-Trp (D or L);  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(33)  
 <223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-

## sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 262

Xaa Phe Gly His Xaa Xaa Cys Thr Xaa Xaa Leu Gly Xaa Cys Xaa Val  
 1 5 10 15

Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu  
 20 25 30

Xaa

&lt;210&gt; 263

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; Conus wittigi

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(231)

&lt;400&gt; 263

ggatcc atg aaa ctg acg tgt gtg gtg atc atc gcc ttg ctg ttc ctg 48  
 Met Lys Leu Thr Cys Val Val Ile Ile Ala Leu Leu Phe Leu  
 1 5 10

acg gcc tgt cag ctc att acg gct gat tac tcc aga gat gag cag tct 96  
 Thr Ala Cys Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Glu Gln Ser  
 15 20 25 30

ggc agt aca gtg cgg ttt cta gac aga cca cgg cgt ttt ggt tcg ttc 144  
 Gly Ser Thr Val Arg Phe Leu Asp Arg Pro Arg Arg Phe Gly Ser Phe  
 35 40 45

ata ccg tgc gcc cgt tta ggt gaa cca tgt acc ata tgc tgc cgt cct 192  
 Ile Pro Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile Cys Cys Arg Pro  
 50 55 60

ttg agg tgc cgt gaa agc gga aca ccc aca tgt caa gtg tgattgtctg 241  
 Leu Arg Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln Val  
 65 70 75

gcatctgata tttccctct gtgccctacc ctcttttgcc tgagtcaccc atacctgtgc 301

tcgag 306

&lt;210&gt; 264

&lt;211&gt; 75

&lt;212&gt; PRT

&lt;213&gt; Conus wittigi

&lt;400&gt; 264

Met Lys Leu Thr Cys Val Val Ile Ile Ala Leu Leu Phe Leu Thr Ala  
 1 5 10 15

Cys Gln Leu Ile Thr Ala Asp Tyr Ser Arg Asp Glu Gln Ser Gly Ser  
 20 25 30

Thr Val Arg Phe Leu Asp Arg Pro Arg Arg Phe Gly Ser Phe Ile Pro  
 35 40 45

Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile Cys Cys Arg Pro Leu Arg  
50 55 60

Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln Val  
65 70 75

<210> 265

<211> 33

<212> PRT

<213> Conus wittigi

<220>

<221> PEPTIDE

<222> (1)..(33)

<223> Xaa at residues 12 and 25 is Glu or gamma-carboxy-Glu; Xaa at residues 6, 13, 20 and 29 is Pro or hydroxy-Pro

<400> 265

Phe Gly Ser Phe Ile Xaa Cys Ala Arg Leu Gly Xaa Xaa Cys Thr Ile  
1 5 10 15

Cys Cys Arg Xaa Leu Arg Cys Arg Xaa Ser Gly Thr Xaa Thr Cys Gln  
20 25 30

Val

<210> 266

<211> 381

<212> DNA

<213> Conus regius

<220>

<221> CDS

<222> (7)..(240)

<400> 266

ggatcc atg aaa ctg acg tgc gtg gtg atc atg gcc tcg ctg ttc ctg 48  
Met Lys Leu Thr Cys Val Val Ile Met Ala Ser Leu Phe Leu  
1 5 10

gcg gcc tgt caa ttc ctt aca gct gga ggt gac tca aga agt aag cag 96  
Ala Ala Cys Gln Phe Leu Thr Ala Gly Gly Asp Ser Arg Ser Lys Gln  
15 20 25 30

cgg tat cct gat tgg agg ctg ggc tac cga aag tcc aag ttg atg gct 144  
Arg Tyr Pro Asp Trp Arg Leu Gly Tyr Arg Lys Ser Lys Leu Met Ala  
35 40 45

aag aag acg tgc ctg gaa cat aac aaa cta tgt tgg tat gat aga gac 192  
Lys Lys Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp  
50 55 60

tgc tgc acc ata tat tgt aat gaa aac aaa tgc ggc gtg aaa cct caa 240  
Cys Cys Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln  
65 70 75

tgaatgtttc acacacacac acacacacac acacacacac acacacacac acacacacac 300

acacacacac atctggcgtc tgaccattcc ccctctgtgc tctatcctct tgttcctgag 360

tcatccatac ctgtgctcga g

381

&lt;210&gt; 267

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus regius

&lt;400&gt; 267

Met Lys Leu Thr Cys Val Val Ile Met Ala Ser Leu Phe Leu Ala Ala  
 1 5 10 15

Cys Gln Phe Leu Thr Ala Gly Gly Asp Ser Arg Ser Lys Gln Arg Tyr  
 20 25 30

Pro Asp Trp Arg Leu Gly Tyr Arg Lys Ser Lys Leu Met Ala Lys Lys  
 35 40 45

Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp Cys Cys  
 50 55 60

Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln  
 65 70 75

&lt;210&gt; 268

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Conus regius

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(30)

<223> Xaa at residues 4 and 22 is Glu or gamma-carboxy-Glu; Xaa at  
 residue 29 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L)  
 or bromo-Trp (D or L); Xaa at residues 11 and 19 is Tyr, 125I-Tyr,  
 mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

&lt;400&gt; 268

Thr Cys Leu Xaa His Asn Lys Leu Cys Xaa Xaa Asp Arg Asp Cys Cys  
 1 5 10 15

Thr Ile Xaa Cys Asn Xaa Asn Lys Cys Gly Val Lys Xaa Gln  
 20 25 30

&lt;210&gt; 269

&lt;211&gt; 285

&lt;212&gt; DNA

&lt;213&gt; Conus radiatus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(225)

&lt;400&gt; 269

atc atg cag aaa ctg aca atc ctg ctt ctt gtt gct gct ata ctg atg 48  
 Ile Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met  
 1 5 10 15

tgc acc cag gtc ctg att caa ggt ggt gga gaa aaa cgc caa aaa gtc 96  
 Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val

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                20                25                30
aac att ttt tca aaa aga aag aca gat gct gag acc tgg tgg gag ggc      144
Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly
          35                40                45

gaa tgc tct aat tgg tta gga agt tgt tcg acg ccc tca aat tgc tgt      192
Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys
          50                55                60

ctc aag agt tgt aat ggg cac tgc aca ttg tgg tgatgaactc tgaccacaaa      245
Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
65                70                75

gccatccaac atcaccgctc tcctcttcag agtcttcaag      285

<210> 270
<211> 75
<212> PRT
<213> Conus radiatus

<400> 270
Ile Met Gln Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Ile Leu Met
1                5                10                15

Ser Thr Gln Val Leu Ile Gln Gly Gly Gly Glu Lys Arg Gln Lys Val
          20                25                30

Asn Ile Phe Ser Lys Arg Lys Thr Asp Ala Glu Thr Trp Trp Glu Gly
          35                40                45

Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro Ser Asn Cys Cys
          50                55                60

Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp
65                70                75

<210> 271
<211> 31
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 3 and 5 is Glu or gamma-carboxy-Glu; Xaa at
      residue 16 is Pro or hydroxy-Pro; Xaa at residues 1,2, 9 and 31
      is Trp (D or L) or bromo-Trp (D or L)

<400> 271
Xaa Xaa Xaa Gly Xaa Cys Ser Asn Xaa Leu Gly Ser Cys Ser Thr Xaa
1                5                10                15

Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Xaa
          20                25                30

<210> 272
<211> 296
<212> DNA
<213> Conus radiatus

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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(237)

&lt;400&gt; 272

atc	atg	cag	aaa	ctg	ata	atc	ctg	ctt	ctt	gtt	gct	gct	gta	ctg	atg	48
Met	Gln	Lys	Leu	Ile	Ile	Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met		
1				5					10					15		

tcc	acc	cag	gcc	ctg	att	caa	ggg	ggg	gga	gga	aaa	cgc	caa	cag	gca	96
Ser	Thr	Gln	Ala	Leu	Ile	Gln	Gly	Gly	Gly	Gly	Lys	Arg	Gln	Gln	Ala	
				20					25					30		

aag	agc	aag	tat	ttt	tcc	gaa	aga	aag	gca	cct	gct	aag	cgt	tgg	ttt	144
Lys	Ser	Lys	Tyr	Phe	Ser	Glu	Arg	Lys	Ala	Pro	Ala	Lys	Arg	Trp	Phe	
			35					40					45			

gga	cac	gaa	gaa	tgc	act	tat	tgg	ttg	ggg	cct	tgt	gag	gtg	gac	gac	192
Gly	His	Glu	Glu	Cys	Thr	Tyr	Trp	Leu	Gly	Pro	Cys	Glu	Val	Asp	Asp	
		50					55					60				

acg	tgt	tgt	tct	gcc	agt	tgt	gag	tcc	aag	ttc	tgc	ggg	ttg	tgg		237
Thr	Cys	Cys	Ser	Ala	Ser	Cys	Glu	Ser	Lys	Phe	Cys	Gly	Leu	Trp		
	65					70				75						

tgatggacac	tgaccacaag	tcatactaca	tcgccactct	cctgttcaga	gtcttcaag	296
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&lt;210&gt; 273

&lt;211&gt; 78

&lt;212&gt; PRT

&lt;213&gt; Conus radiatus

&lt;400&gt; 273

Met	Gln	Lys	Leu	Ile	Ile	Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met	Ser
1				5					10					15	

Thr	Gln	Ala	Leu	Ile	Gln	Gly	Gly	Gly	Gly	Lys	Arg	Gln	Gln	Ala	Lys
			20					25					30		

Ser	Lys	Tyr	Phe	Ser	Glu	Arg	Lys	Ala	Pro	Ala	Lys	Arg	Trp	Phe	Gly
		35					40					45			

His	Glu	Glu	Cys	Thr	Tyr	Trp	Leu	Gly	Pro	Cys	Glu	Val	Asp	Asp	Thr
	50					55					60				

Cys	Cys	Ser	Ala	Ser	Cys	Glu	Ser	Lys	Phe	Cys	Gly	Leu	Trp
65					70				75				

&lt;210&gt; 274

&lt;211&gt; 33

&lt;212&gt; PRT

&lt;213&gt; Conus radiatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(33)

<223> Xaa at residues 5, 6, 15 and 26 is Glu or gamma-carboxy-Glu; Xaa at residue 13 is Pro or hydroxy-Pro; Xaa at residues 1, 10 and 33 is Trp (D or L) or bromo-Trp (D or L);

<220>  
 <221> PEPTIDE  
 <222> (1)..(33)  
 <223> Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
 O-sulpho-Tyr or O-phospho-Tyr

<400> 274  
 Xaa Phe Gly His Xaa Xaa Cys Thr Xaa Xaa Leu Gly Xaa Cys Xaa Val  
 1 5 10 15

Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu  
 20 25 30

Xaa

<210> 275  
 <211> 387  
 <212> DNA  
 <213> Conus spurius

<220>  
 <221> CDS  
 <222> (21)..(212)

<400> 275  
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu  
 1 5 10

ctg ctg att cca tct gca cct agc act gat gcc cga ccg aag acc aaa 101  
 Leu Leu Ile Pro Ser Ala Pro Ser Thr Asp Ala Arg Pro Lys Thr Lys  
 15 20 25

gat gat gtg cgc ctg gca tct ttc cac ggt aag gca aag cga acc cta 149  
 Asp Asp Val Arg Leu Ala Ser Phe His Gly Lys Ala Lys Arg Thr Leu  
 30 35 40

caa ata cct agg ggg aat atc cac tgt tgc aca aaa tat cag ccg tgc 197  
 Gln Ile Pro Arg Gly Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys  
 45 50 55

tgt tct tca cca tca taaagggaaa tgactttgat gagaccctg cgaactgtcc 252  
 Cys Ser Ser Pro Ser  
 60

ctggatgtga aatttggaac cgagactgtt cctttcgcgc gtgttcgtgg aatttcgaat 312

ggtcgttaat aacacgctgc ctcttgcaaa ctacaatctc tctgtccttt atctgtggac 372

tgcatgtcaa cactg 387

<210> 276  
 <211> 64  
 <212> PRT  
 <213> Conus spurius

<400> 276  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Pro Ser  
 1 5 10 15

Ala Pro Ser Thr Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Arg Leu  
20 25 30

Ala Ser Phe His Gly Lys Ala Lys Arg Thr Leu Gln Ile Pro Arg Gly  
35 40 45

Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys Cys Ser Ser Pro Ser  
50 55 60

<210> 277

<211> 17

<212> PRT

<213> Conus spurius

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residues 11 and 16 is Pro or hydroxy-Pro; Xaa at residue 9  
is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Tyr

<400> 277

Gly Asn Ile His Cys Cys Thr Lys Xaa Gln Xaa Cys Cys Ser Ser Xaa  
1 5 10 15  
Ser

<210> 278

<211> 206

<212> DNA

<213> Conus nobilis

<220>

<221> CDS

<222> (1)..(183)

<400> 278

atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48  
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

gca cca agc gtt gat gcc cga ccg aag acc aaa gat gat gtg ctc cgg 96  
Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Leu Arg  
20 25 30

gca tct ttc cgc gat aat gca aag agt acc cta caa aga ctt tgg aac 144  
Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Trp Asn  
35 40 45

aaa cgc atc tgc tgc ccc ata att ctt tgg tgc tgt ggt taaccagcat 193  
Lys Arg Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys Gly  
50 55 60

gaagttccca gga 206

<210> 279

<211> 61

<212> PRT

<213> Conus nobilis



&lt;400&gt; 279

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Leu Arg  
 20 25 30

Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Trp Asn  
 35 40 45

Lys Arg Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys Gly  
 50 55 60

&lt;210&gt; 280

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Conus nobilis

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(10)

<223> Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp  
 (D or L) or bromo-Trp (D or L)

&lt;400&gt; 280

Ile Cys Cys Xaa Ile Ile Leu Xaa Cys Cys  
 1 5 10

&lt;210&gt; 281

&lt;211&gt; 205

&lt;212&gt; DNA

&lt;213&gt; Conus betulinus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(183)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(205)

&lt;223&gt; n is unknown

&lt;400&gt; 281

atg cgc tgt ctc cca gtc ttc atc att ctt ctg gtg ctg att gca tct 48  
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Val Leu Ile Ala Ser  
 1 5 10 15

gca cct acc gtt gat gcc cga cca aag atc gaa gat gat gag tcc ctg 96  
 Ala Pro Thr Val Asp Ala Arg Pro Lys Ile Glu Asp Asp Glu Ser Leu  
 20 25 30

gca tct ttc cat gnt cat naa cca cca tna nng ntn can ctt ttg aac 144  
 Ala Ser Phe His Xaa His Xaa Pro Pro Xaa Xaa Xaa Thr Leu Leu Asn  
 35 40 45

aaa cgc aat tgc tgc cca gac tct cct ccg tgc tgt cat taaccagcat 193  
 Lys Arg Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His  
 50 55 60

gaaggttcag ga 205

<210> 282  
 <211> 61  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> misc\_feature  
 <222> (1)..(61)  
 <223> Xaa is unknown

<400> 282  
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Val Leu Ile Ala Ser  
 1 5 10 15  
 Ala Pro Thr Val Asp Ala Arg Pro Lys Ile Glu Asp Asp Glu Ser Leu  
 20 25 30  
 Ala Ser Phe His Xaa His Xaa Pro Pro Xaa Xaa Xaa Thr Leu Leu Asn  
 35 40 45  
 Lys Arg Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His  
 50 55 60

<210> 283  
 <211> 11  
 <212> PRT  
 <213> Conus betulinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa at residues 4, 7 and 8 is Pro or hydroxy-Pro

<400> 283  
 Asn Cys Cys Xaa Asp Ser Xaa Xaa Cys Cys His  
 1 5 10

<210> 284  
 <211> 569  
 <212> DNA  
 <213> Conus purpurascens

<400> 284  
 ggaattccaa atgatgtaat tactgactac atggtcata tagtataccca ttgaaaaatt 60  
 tctatgacat ttcagttggt agatcatcca gttccacaga tggaaagaca gagagatagt 120  
 agcttgcaag tggcagcgtg ttgttaacga ccattcgaca ttccatgaac acgtgtgaaa 180  
 ggagcagtct gctttccaaa tctgacatcc agggacagtt tgcaggggtc tcatccaaag 240  
 tcatcttctt ttatcccaaa gtacagcacc gcatctgttt tggacagcaa ccgcgtttct 300  
 tccaaaatct ttgtagggtt ctttttgc atctgtggaa agatgccagg ggcatatcat 360  
 ctttgggtctt cggatgagca tcaacgcaag gtgcagatgg aatcagcagc agaagaatga 420  
 cgaagactgg cagacagcgc attctgcttg tagtcagctt ccgaattcca agccgaattc 480  
 tgcatgatc catcacactg gcggccgctc gagcatgcat ctagagggcc caattcgccc 540

tatagtgagt cgtatgacaa ttcactggc

569

<210> 285

<211> 63

<212> PRT

<213> Conus purpurascens

<400> 285

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Pro Ser  
1 5 10 15

Ala Pro Cys Val Asp Ala His Pro Lys Thr Lys Asp Asp Met Pro Leu  
20 25 30

Ala Ser Phe His Asp Asn Ala Lys Gly Thr Leu Gln Arg Phe Trp Lys  
35 40 45

Lys Arg Gly Cys Cys Pro Lys Gln Met Arg Cys Cys Thr Leu Gly  
50 55 60

<210> 286

<211> 12

<212> PRT

<213> Conus purpurascens

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 4 is Pro or hydroxy-Pro

<400> 286

Gly Cys Cys Xaa Lys Gln Met Arg Cys Cys Thr Leu  
1 5 10

<210> 287

<211> 221

<212> DNA

<213> Conus ammiralis

<220>

<221> CDS

<222> (21)..(206)

<400> 287

ggaagctgac tacaagcaga atg cac tgt ctc cca gtc gtc gtc att ctt ctg 53  
Met His Cys Leu Pro Val Val Val Ile Leu Leu  
1 5 10

ctg ctg act gca tct ggt gga cct agc gtt gat gcc cga ctg aag acc 101  
Leu Leu Thr Ala Ser Gly Gly Pro Ser Val Asp Ala Arg Leu Lys Thr  
15 20 25

aaa gat gat gtg ccc ctg tca tct ttc cgc gat aat aca aag agt atc 149  
Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Ile  
30 35 40

cta caa aga ctt tgg aag cga ggc aac tgc tgt gaa ttt tgg gag ttt 197  
Leu Gln Arg Leu Trp Lys Arg Gly Asn Cys Cys Glu Phe Trp Glu Phe  
45 50 55

tgc tgt gat taaccagcat gaagg  
Cys Cys Asp  
60

221

<210> 288  
<211> 62  
<212> PRT  
<213> Conus ammiralis

<400> 288  
Met His Cys Leu Pro Val Val Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15  
Gly Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro  
20 25 30  
Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Ile Leu Gln Arg Leu Trp  
35 40 45  
Lys Arg Gly Asn Cys Cys Glu Phe Trp Glu Phe Cys Cys Asp  
50 55 60

<210> 289  
<211> 12  
<212> PRT  
<213> Conus ammiralis

<220>  
<221> PEPTIDE  
<222> (1)..(12)  
<223> Xaa at residues 5 and 8 is Glu or gamma-carboxy-Glu; Xaa at  
residue 7 is Trp (D or L) or bromo-Trp (D or L)

<400> 289  
Gly Asn Cys Cys Xaa Phe Xaa Xaa Phe Cys Cys Asp  
1 5 10

<210> 290  
<211> 209  
<212> DNA  
<213> Conus dalli

<220>  
<221> CDS  
<222> (21)..(194)

<400> 290  
ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53  
Met His Cys Leu Pro Val Phe Val Ile Leu Leu  
1 5 10  
ctg ctg act gca tct gga cct agc gtt gat gcc caa ccg aag acc gaa 101  
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Gln Pro Lys Thr Glu  
15 20 25  
gtt gat gtg ccc ctg tca tct ttc cgc gat aat gca aag cgt gcc cta 149  
Val Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Arg Ala Leu  
30 35 40  
caa aga ctt ccg cgt tgc tgt gaa tat tgg aag ttg tgc tgt ggt 194

Gln Arg Leu Pro Arg Cys Cys Glu Tyr Trp Lys Leu Cys Cys Gly  
45 50 55  
taaccagcat gaagg 209

<210> 291  
<211> 58  
<212> PRT  
<213> Conus dalli

<400> 291  
Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15  
Gly Pro Ser Val Asp Ala Gln Pro Lys Thr Glu Val Asp Val Pro Leu  
20 25 30  
Ser Ser Phe Arg Asp Asn Ala Lys Arg Ala Leu Gln Arg Leu Pro Arg  
35 40 45  
Cys Cys Glu Tyr Trp Lys Leu Cys Cys Gly  
50 55

<210> 292  
<211> 9  
<212> PRT  
<213> Conus dalli

<220>  
<221> PEPTIDE  
<222> (1)..(9)  
<223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is  
Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr,  
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Tyr

<400> 292  
Cys Cys Xaa Xaa Xaa Lys Leu Cys Cys  
1 5

<210> 293  
<211> 218  
<212> DNA  
<213> Conus omaria

<220>  
<221> CDS  
<222> (21)..(203)

<400> 293  
ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu  
1 5 10  
ctg cta act gca tct gca cct agc gtt gat gcc cga ccg aag gcc aaa 101  
Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys  
15 20 25  
gat gat gtg ccc ctg gca tct ttc cgt gat aat gca aag agt acc cta 149  
Asp Asp Val Pro Leu Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu  
30 35 40

caa aga ctt cag gac aaa cgc gtt tgc tgt ggc tat aag ttt ttt tgc 197  
 Gln Arg Leu Gln Asp Lys Arg Val Cys Cys Gly Tyr Lys Phe Phe Cys  
     45                    50                    55

tgt cgt taaccagcat gaagg 218  
 Cys Arg  
 60

<210> 294  
 <211> 61  
 <212> PRT  
 <213> Conus omaria

<400> 294  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1                    5                    10                    15

Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys Asp Asp Val Pro Leu  
                     20                    25                    30

Ala Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp  
                     35                    40                    45

Lys Arg Val Cys Cys Gly Tyr Lys Phe Phe Cys Cys Arg  
                     50                    55                    60

<210> 295  
 <211> 11  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,  
       O-sulpho-Tyr or O-phospho-Tyr

<400> 295  
 Val Cys Cys Gly Xaa Lys Phe Phe Cys Cys Arg  
 1                    5                    10

<210> 296  
 <211> 212  
 <212> DNA  
 <213> Conus aulicus

<220>  
 <221> CDS  
 <222> (21)..(197)

<400> 296  
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
                     Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu  
                     1                    5                    10

ctg ctg act gca tct gca cct aac gtt gat gcc caa ccg aag acc aaa 101  
 Leu Leu Thr Ala Ser Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys  
                     15                    20                    25

gat gat gtg ccc ctg gca tct ttg cac gat gat gca aag agt gca cta 149

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Asp Asp Val Pro Leu Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu
 30 35 40
caa cat tgg aac caa cgc tgc tgc ccc atg atc tat tgg tgc tgt agt 197
Gln His Trp Asn Gln Arg Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
 45 50 55
taaccagcat gaagg 212

<210> 297
<211> 59
<212> PRT
<213> Conus aulicus

<400> 297
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser
 1 5 10 15
Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu Gln His Trp Asn Gln
 35 40 45
Arg Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser
 50 55

<210> 298
<211> 10
<212> PRT
<213> Conus aulicus

<220>
<221> PEPTIDE
<222> (1)..(10)
<223> Xaa at residue 3 is Pro or hydroxy-Pro; Xaa at residue 7 is Trp
(D or L) or bromo-Trp (D or L); Xaa at residue 6 is Tyr, 125I-Tyr,
mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 298
Cys Cys Xaa Met Ile Xaa Xaa Cys Cys Ser
 1 5 10

<210> 299
<211> 212
<212> DNA
<213> Conus aulicus

<220>
<221> CDS
<222> (21)..(197)

<400> 299
ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53
Met His Cys Leu Pro Val Phe Val Ile Leu Leu
 1 5 10
ctg ctg act gca tct gca cct aac gtt gat gcc caa ccg aag acc aaa 101
Leu Leu Thr Ala Ser Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys
 15 20 25

```

gat gat gtg ccc ctg gca tct ttg cac gat gat gca aag agt gca cta 149  
 Asp Asp Val Pro Leu Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu  
           30                          35                          40

caa cat tgg aac caa cgc tgc tgc ccc gag atc tat tgg tgc tgt agt 197  
 Gln His Trp Asn Gln Arg Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser  
           45                          50                          55

taaccagcat gaagg 212

<210> 300  
 <211> 59  
 <212> PRT  
 <213> Conus aulicus

<400> 300  
 Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
   1                          5                          10                          15

Ala Pro Asn Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu  
           20                          25                          30

Ala Ser Leu His Asp Asp Ala Lys Ser Ala Leu Gln His Trp Asn Gln  
           35                          40                          45

Arg Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser  
           50                          55

<210> 301  
 <211> 10  
 <212> PRT  
 <213> Conus aulicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(10)  
 <223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residue 3 is  
       Pro or hydroxy-Pro; Xaa at residue 7 is Trp (D or L) or bromo-  
       Trp (D or L); Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr,  
       di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 301  
 Cys Cys Xaa Xaa Ile Xaa Xaa Cys Cys Ser  
   1                          5                          10

<210> 302  
 <211> 215  
 <212> DNA  
 <213> Conus ammiralis

<220>  
 <221> CDS  
 <222> (21)..(200)

<400> 302  
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
                           Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu  
                           1                          5                          10



ctg ctg att gca tct gca cct agc gtt gat gcc caa ccg aag acc aaa 101  
 Leu Leu Ile Ala Ser Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys  
           15                                  20                                  25

gat gat gtg tcc ctg gca tct ttg cac gat aat ata aag agt act cta 149  
 Asp Asp Val Ser Leu Ala Ser Leu His Asp Asn Ile Lys Ser Thr Leu  
           30                                  35                                  40

caa aca ctt tgg aac aaa cgc tgc tgc ccc cct gtg att tgg tgc tgt 197  
 Gln Thr Leu Trp Asn Lys Arg Cys Cys Pro Pro Val Ile Trp Cys Cys  
           45                                  50                                  55

ggt taaccagcat aaagg 215  
 Gly  
 60

<210> 303  
 <211> 60  
 <212> PRT  
 <213> Conus ammiralis

<400> 303  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser  
 1                                  5                                  10                                  15

Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Ser Leu  
           20                                  25                                  30

Ala Ser Leu His Asp Asn Ile Lys Ser Thr Leu Gln Thr Leu Trp Asn  
           35                                  40                                  45

Lys Arg Cys Cys Pro Pro Val Ile Trp Cys Cys Gly  
           50                                  55                                  60

<210> 304  
 <211> 9  
 <212> PRT  
 <213> Conus ammiralis

<220>  
 <221> PEPTIDE  
 <222> (1)..(9)  
 <223> Xaa at residues 3 and 4 is Pro or hydroxy-Pro; Xaa at residue 7  
       is Trp (D or L) or bromo-Trp (D or L)

<400> 304  
 Cys Cys Xaa Xaa Val Ile Xaa Cys Cys  
 1                                  5

<210> 305  
 <211> 215  
 <212> DNA  
 <213> Conus aulicus

<220>  
 <221> CDS  
 <222> (21)..(200)

<400> 305  
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
                                   Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu

	1	5	10	
ctg ctg act gca tct gga cct agc gtt gat gcc cga ccg aag acc aaa				101
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Lys	15	20	25	
gat gat gtg cct ctg tca tct ttc cgc gat aac gca aag agt atc cta				149
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Ile Leu	30	35	40	
caa aga cgt tgg aac aac tat tgc tgc acg aat gag ctt tgg tgc tgt				197
Gln Arg Arg Trp Asn Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys	45	50	55	
ggt taaccagcat gaagg				215
Gly				
60				
<210>	306			
<211>	60			
<212>	PRT			
<213>	Conus aulicus			
<400>	306			
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser				
1 5 10 15				
Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Val Pro Leu	20	25	30	
Ser Ser Phe Arg Asp Asn Ala Lys Ser Ile Leu Gln Arg Arg Trp Asn	35	40	45	
Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys Gly	50	55	60	
<210>	307			
<211>	13			
<212>	PRT			
<213>	Conus aulicus			
<220>				
<221>	PEPTIDE			
<222>	(1)..(13)			
<223>	Xaa at residue 9 is Glu or gamma-carboxy-Glu; Xaa at residues 1 and 11 is Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr			
<400>	307			
Xaa Asn Asn Xaa Cys Cys Thr Asn Xaa Leu Xaa Cys Cys				
1 5 10				
<210>	308			
<211>	218			
<212>	DNA			
<213>	Conus dalli			
<220>				
<221>	CDS			

<222> (21)..(203)

<400> 308

ggaagctgac tacaagcaga atg cac tgt ctc cca gtc ttc gtc att ctt ctg 53  
Met His Cys Leu Pro Val Phe Val Ile Leu Leu  
1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc cga ccg aag acc gaa 101  
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Glu  
15 20 25

gat gat gtg ccc ctg tca tct ttc cgc gat aat aca aag agt acc cta 149  
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Thr Lys Ser Thr Leu  
30 35 40

caa aga ctt ttg aag cca gtc aac tgc tgt cct att gat caa tct tgc 197  
Gln Arg Leu Leu Lys Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys  
45 50 55

tgt tct taaccagcat gaagg 218  
Cys Ser  
60

<210> 309

<211> 61

<212> PRT

<213> Conus dalli

<400> 309

Met His Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

Gly Pro Ser Val Asp Ala Arg Pro Lys Thr Glu Asp Asp Val Pro Leu  
20 25 30

Ser Ser Phe Arg Asp Asn Thr Lys Ser Thr Leu Gln Arg Leu Leu Lys  
35 40 45

Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys Cys Ser  
50 55 60

<210> 310

<211> 13

<212> PRT

<213> Conus dalli

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1 and 6 is Pro or hydroxy-Pro

<400> 310

Xaa Val Asn Cys Cys Xaa Ile Asp Gln Ser Cys Cys Ser  
1 5 10

<210> 311

<211> 239

<212> DNA

<213> Conus consors

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<220>
<221> CDS
<222> (7)..(228)

<400> 311
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc      48
      Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
        1             5             10

      gtt tcc atc cct tca gat cgt gca tct gaa ggc agg aat gcc gta gtc      96
      Val Ser Ile Pro Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Val Val
      15             20             25             30

      cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt      144
      His Glu Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys
                35             40             45

      ggt tat gat ccg atg aca ata tgc cct cct tgc atg tgc act cat tcc      192
      Gly Tyr Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser
                50             55             60

      tgt cca cca aaa aga aaa cca ggc cgc aga aac gac tgatgctcga g      239
      Cys Pro Pro Lys Arg Lys Pro Gly Arg Arg Asn Asp
                65             70

<210> 312
<211> 74
<212> PRT
<213> Conus consors

<400> 312
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1             5             10             15

Ile Pro Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Val Val His Glu
20             25             30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr
35             40             45

Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro
50             55             60

Pro Lys Arg Lys Pro Gly Arg Arg Asn Asp
65             70

<210> 313
<211> 36
<212> PRT
<213> Conus consors

<220>
<221> PEPTIDE
<222> (1)..(36)
<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2,
      17, 22, 23, 31, 32 and 36 is Pro or hydroxy-Pro; Xaa at residue
      15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
      or O-phospho-Tyr

<400> 313

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Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp  
1 5 10 15

Xaa Met Thr Ile Cys Xaa Xaa Cys Met Cys Thr His Ser Cys Xaa Xaa  
20 25 30

Lys Arg Lys Xaa  
35

<210> 314

<211> 272

<212> DNA

<213> *Conus aurisiacus*

<220>

<221> CDS

<222> (7)..(237)

<400> 314

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48  
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
1 5 10

gtt tcc atc cct tca gat cgt gca tct gat ggc agg aat gcc gca gtc 96  
Val Ser Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val  
15 20 25 30

aac gag aga caa tct tgg ctg gtc cct tcg aca atc acg act tgc tgt 144  
Asn Glu Arg Gln Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys  
35 40 45

gga tat gat ccg ggg aca atg tgc cct cct tgc agg tgc aat aat acc 192  
Gly Tyr Asp Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr  
50 55 60

tgt aaa cca aaa aaa cca aaa cca gga aaa ggc cgc aga aac gac 237  
Cys Lys Pro Lys Lys Pro Lys Pro Gly Lys Gly Arg Arg Asn Asp  
65 70 75

tgatgctcca ggaccctctg aaccacgacc tcgag 272

<210> 315

<211> 77

<212> PRT

<213> *Conus aurisiacus*

<400> 315

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Val Asn Glu  
20 25 30

Arg Gln Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr  
35 40 45

Asp Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr Cys Lys  
50 55 60

Pro Lys Lys Pro Lys Pro Gly Lys Gly Arg Arg Asn Asp



<213> Conus consors

<400> 318

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
1 5 10 15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Val Val His Glu  
20 25 30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr  
35 40 45

Asp Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser Cys Pro  
50 55 60

His Gln Arg Lys Lys Pro Gly Arg Arg Asn Asp  
65 70 75

<210> 319

<211> 37

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2, 17, 22, 31 and 37 is Pro or hydroxy-Pro; Xaa at residue 20 is Trp (D or L) or bromo-Trp (D or L);

<220>

<221> PEPTIDE

<222> (1)..(37)

<223> Xaa at residues 15 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 319

Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp  
1 5 10 15

Xaa Met Thr Xaa Cys Xaa Ser Cys Met Cys Thr Xaa Ser Cys Xaa His  
20 25 30

Gln Arg Lys Lys Xaa  
35

<210> 320

<211> 260

<212> DNA

<213> Conus magus

<220>

<221> CDS

<222> (7)..(231)

<220>

<221> misc\_feature

<222> (1)..(260)

<223> n is unknown

<400> 320  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc agt gtc 48  
           Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ser Val  
           1                  5                  10

gtt tcc atc cct tca gat cgt gca tct gat ggc ggg aat gcc gta gtc 96  
 Val Ser Ile Pro Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Val Val  
 15                  20                  25                  30

cac gag aga gcg cct gag ctg gtc gtt acg gcc acc acg act tgc tgt 144  
 His Glu Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys  
                   35                  40                  45

ggt tat gat ccg atg aca ata tgc cct ccc tgc atg tgc act cat tcc 192  
 Gly Tyr Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser  
                   50                  55                  60

tgt cca cca aaa gga aaa cca ggc cgc agg aac gac tga tgtccaggac 241  
 Cys Pro Pro Lys Gly Lys Pro Gly Arg Arg Asn Asp  
           65                  70

ctctgaacca cgacncgag 260

<210> 321  
 <211> 74  
 <212> PRT  
 <213> Conus magus

<400> 321  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ser Val Val Ser  
 1                  5                  10                  15

Ile Pro Ser Asp Arg Ala Ser Asp Gly Gly Asn Ala Val Val His Glu  
                   20                  25                  30

Arg Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr  
                   35                  40                  45

Asp Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro  
           50                  55                  60

Pro Lys Gly Lys Pro Gly Arg Arg Asn Asp  
 65                  70

<210> 322  
 <211> 36  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(36)  
 <223> Xaa at residue 3 is Glu or gamma-carboxy-Glu; Xaa at residues 2,  
 17, 22, 23, 31, 32 and 36 is Pro or hydroxy-Pro; Xaa at residue  
 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 322  
 Ala Xaa Xaa Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Xaa Asp



1                    5                    10                    15  
Xaa Met Thr Ile Cys Xaa Xaa Cys Met Cys Thr His Ser Cys Xaa Xaa  
                    20                    25                    30

Lys Gly Lys Xaa  
35

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<210> 323
<211> 251
<212> DNA
<213> Conus aurisiacus
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<220>
<221> CDS
<222> (23)..(202)
```

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<400> 323
gaattcggccc ttgaggatcc gt gtg gtt ctg ggt cca gaa cct gat ggc agg      52
                        Val Val Leu Gly Pro Glu Pro Asp Gly Arg
                        1          5          10
```

aat gcc gca gtc aac gag aga cag aaa tgg ctg gtc cat tcg aaa atc 100  
Asn Ala Ala Val Asn Glu Arg Gln Lys Trp Leu Val His Ser Lys Ile  
15 20 25

acg tat tgc tgt ggt tat aat aag atg gac atg tgc cct cct tgc atg 148  
Thr Tyr Cys Cys Gly Tyr Asn Lys Met Asp Met Cys Pro Pro Cys Met  
30 35 40

tgc	act	tat	tcc	tgt	ccc	ccc	cta	aaa	aaa	aaa	aga	cca	ggc	cgc	aga	196
Cys	Thr	Tyr	Ser	Cys	Pro	Pro	Leu	Lys	Lys	Lys	Arg	Pro	Gly	Arg	Arg	
		45					50					55				

aac gac tgatgctcca ggaccctctg aaccacgacc tcgagcgaag ggcgaaattc 251  
Asn Asp  
60

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<210> 324
<211> 60
<212> PRT
<213> Conus aurisiacus
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<400> 324
Val Val Leu Gly Pro Glu Pro Asp Gly Arg Asn Ala Ala Val Asn Glu
1          5          10          15
```

Arg Gln Lys Trp Leu Val His Ser Lys Ile Thr Tyr Cys Cys Gly Tyr  
20 25 30

Asn Lys Met Asp Met Cys Pro Pro Cys Met Cys Thr Tyr Ser Cys Pro  
35 40 45

Pro Leu Lys Lys Lys Arg Pro Gly Arg Arg Asn Asp  
50 55 60

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<210> 325
<211> 38
<212> PRT
<213> Conus aurisiacus
```

<220>  
 <221> PEPTIDE  
 <222> (1)..(38)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 22, 23, 31, 32 and 38 is Pro or hydroxy-Pro; Xaa at residue 3 is Trp (D or L) or bromo-Trp (D or L); Xaa at residues 11, 15 and 28 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 325  
 Xaa Lys Xaa Leu Val His Ser Lys Ile Thr Xaa Cys Cys Gly Xaa Asn  
 1 5 10 15  
 Lys Met Asp Met Cys Xaa Xaa Cys Met Cys Thr Xaa Ser Cys Xaa Xaa  
 20 25 30  
 Leu Lys Lys Lys Arg Xaa  
 35

<210> 326  
 <211> 212  
 <212> DNA  
 <213> Conus aurisiacus

<220>  
 <221> CDS  
 <222> (23)..(163)

<400> 326  
 gaattcgccc ttgaggatcc gt gtg gtt ctg ggt cca gca ttt gat ggc agg 52  
 Val Val Leu Gly Pro Ala Phe Asp Gly Arg  
 1 5 10  
 aat gcc gca gtc aac gag aga gcg cct tgg acg gtc gtt acg gcc acc 100  
 Asn Ala Ala Val Asn Glu Arg Ala Pro Trp Thr Val Val Thr Ala Thr  
 15 20 25  
 acg aat tgc tgc ggt att acc ggg cca ggc tgc ctt cct tgc cgt tgt 148  
 Thr Asn Cys Cys Gly Ile Thr Gly Pro Gly Cys Leu Pro Cys Arg Cys  
 30 35 40  
 act caa aca tgt ggc tgatgctcca ggaccctctg aaccacgacc tcgagcgaag 203  
 Thr Gln Thr Cys Gly  
 45  
 ggcgaaattc 212

<210> 327  
 <211> 47  
 <212> PRT  
 <213> Conus aurisiacus

<400> 327  
 Val Val Leu Gly Pro Ala Phe Asp Gly Arg Asn Ala Ala Val Asn Glu  
 1 5 10 15  
 Arg Ala Pro Trp Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile  
 20 25 30  
 Thr Gly Pro Gly Cys Leu Pro Cys Arg Cys Thr Gln Thr Cys Gly  
 35 40 45

<210> 328  
 <211> 29  
 <212> PRT  
 <213> *Conus aurisiacus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residues 2, 18 and 22 is Pro or hydroxy-Pro; Xaa at  
 residue 3 is Trp (D or L) or bromo-Trp (D or L)

<400> 328  
 Ala Xaa Xaa Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile Thr  
 1 5 10 15  
 Gly Xaa Gly Cys Leu Xaa Cys Arg Cys Thr Gln Thr Cys  
 20 25

<210> 329  
 <211> 218  
 <212> DNA  
 <213> *Conus marmoreus*

<220>  
 <221> CDS  
 <222> (21)..(203)

<400> 329  
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttg atc att ctt ctg 53  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu  
 1 5 10  
 ctg ctg act gca tct gca cct ggc gtt gtt gtc cta ccg aag acc gaa 101  
 Leu Leu Thr Ala Ser Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu  
 15 20 25  
 gat gat gtg ccc atg tca tct gtc tac ggt aat gga aag agt atc cta 149  
 Asp Asp Val Pro Met Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu  
 30 35 40  
 cga ggg att ctg agg aac ggt gtt tgc tgt ggc tat aag ttg tgc ctt 197  
 Arg Gly Ile Leu Arg Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys Leu  
 45 50 55  
 cca tgt taaccagcat gaagg 218  
 Pro Cys  
 60

<210> 330  
 <211> 61  
 <212> PRT  
 <213> *Conus marmoreus*

<400> 330  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
 Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met  
 20 25 30

Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg  
           35                          40                          45

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys Leu Pro Cys  
       50                          55                          60

<210> 331

<211> 13

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr,  
       125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
       O-phospho-Tyr

<400> 331

Asn Gly Val Cys Cys Gly Xaa Lys Leu Cys Leu Xaa Cys  
   1                          5                          10

<210> 332

<211> 238

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (28)..(219)

<400> 332

ggaattcgga agctgactac aagcaga atg cgc tgt ctc cca gtc ttc gtc att       54  
                                   Met Arg Cys Leu Pro Val Phe Val Ile  
                                   1                          5

ctt ctg ctg ctg act gca tct gca cct agc gtt gat gcc aaa gtt cat       102  
   Leu Leu Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Lys Val His  
   10                          15                          20                          25

ctg aag acc aaa ggt gat ggg ccc ctg tca tct ttc cga gat aat gca       150  
   Leu Lys Thr Lys Gly Asp Gly Pro Leu Ser Ser Phe Arg Asp Asn Ala  
                           30                          35                          40

aag agt acc cta caa aga ctt cag gac aaa agc act tgc tgt ggc ttt       198  
   Lys Ser Thr Leu Gln Arg Leu Gln Asp Lys Ser Thr Cys Cys Gly Phe  
                           45                          50                          55

aag atg tgt atc cct tgt agt taaccagcat gaaggatcc       238  
   Lys Met Cys Ile Pro Cys Ser  
                           60

<210> 333

<211> 64

<212> PRT

<213> Conus pennaceus

<400> 333

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser

1	5	10	15
Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly	20	25	30
Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu	35	40	45
Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Ser	50	55	60

<210> 334  
 <211> 13  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 334
Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys Ser
1 5 10

<210> 335  
 <211> 231  
 <212> DNA  
 <213> Conus pennaceus

<220>  
 <221> CDS  
 <222> (27)..(212)

<400> 335	
gaattcggaa gctgactaca agcaga atg cgt tgt ctc cca gtc ttc gtc att	53
Met Arg Cys Leu Pro Val Phe Val Ile	
1 5	

ctt ctg ctg ctg act gca tct gga cct agc gtt gat gcc cga ctg aag	101
Leu Leu Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Leu Lys	
10 15 20 25	

acc aaa gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt	149
Thr Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser	
30 35 40	

acc cta caa aga ctt cag gac aaa cgc ctt tgc tgt ggc ttt tgg atg	197
Thr Leu Gln Arg Leu Gln Asp Lys Arg Leu Cys Cys Gly Phe Trp Met	
45 50 55	

tgt att cct tgt aat taaccagcat gaaggatcc	231
Cys Ile Pro Cys Asn	
60	

<210> 336  
 <211> 62  
 <212> PRT  
 <213> Conus pennaceus

&lt;400&gt; 336

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15

Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu  
 20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp  
 35 40 45

Lys Arg Leu Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn  
 50 55 60

&lt;210&gt; 337

&lt;211&gt; 12

&lt;212&gt; PRT

&lt;213&gt; Conus pennaceus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(12)

<223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 6 is Trp  
 (D or L) or bromo-Trp (D or L)

&lt;400&gt; 337

Leu Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Asn  
 1 5 10

&lt;210&gt; 338

&lt;211&gt; 244

&lt;212&gt; DNA

&lt;213&gt; Conus pennaceus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (40)..(225)

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(244)

&lt;223&gt; n is unknown

&lt;400&gt; 338

gaattctccc ttggaattct gaagctgact acaancaga atg cgt tgt ctc cca 54  
 Met Arg Cys Leu Pro  
 1 5

ctc ttc gtc att ctt ctg ctg ctg act gca tct gga cct act gtt gat 102  
 Leu Phe Val Ile Leu Leu Leu Leu Thr Ala Ser Gly Pro Thr Val Asp  
 10 15 20

gcc cga ctg aag acc aaa gat gat gtg ccc ctg tca tct ttc cga gat 150  
 Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu Ser Ser Phe Arg Asp  
 25 30 35

aat gca aag agt acc cta caa aga ctt cag gac aaa agc act tgc tgt 198  
 Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp Lys Ser Thr Cys Cys  
 40 45 50

ggc ttt aag atg tgt att cct tgt ggt taaccagcat gaaggatcc 244

Gly Phe Lys Met Cys Ile Pro Cys Gly  
55 60

<210> 339  
<211> 62  
<212> PRT  
<213> Conus pennaceus

<400> 339  
Met Arg Cys Leu Pro Leu Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

Gly Pro Thr Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu  
20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp  
35 40 45

Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Gly  
50 55 60

<210> 340  
<211> 12  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> PEPTIDE  
<222> (1)..(12)  
<223> Xaa at residue 11 is Pro or hydroxy-Pro

<400> 340  
Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Xaa Cys  
1 5 10

<210> 341  
<211> 250  
<212> DNA  
<213> Conus episcopatus

<220>  
<221> misc\_feature  
<222> (1)..(250)  
<223> n is unknown

<400> 341  
gaattcgccc ttggaattcg gaagctgact acaagcagaa tgcgctgtct ccagctcttc 60  
gtcattcttc tgctgctgac tgcattctgga cctantgttg atgccaaagt tcatctgaag 120  
accaaaggtg atgggccctt gtcattcttc cgagataatg caaagagtac cctacaaaga 180  
cttcaggaca aaagcacttg ctgtggctat aggatgtgtg ttccttgtgg ttaaccagca 240  
tgaaggatcc 250

<210> 342  
<211> 64  
<212> PRT

<213> Conus episcopatus

<400> 342

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

Gly Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly  
20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu  
35 40 45

Gln Asp Lys Ser Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly  
50 55 60

<210> 343

<211> 12

<212> PRT

<213> Conus episcopatus

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr  
, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Tyr

<400> 343

Ser Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys  
1 5 10

<210> 344

<211> 827

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (82)..(264)

<400> 344

ggcgaataca cctggcaggt actcaacgaa cttcaggaca cattcttttc acctggacac 60

tggaaactga caacaggcag a atg cgc tgt ctc cca gtc ttg atc att ctt 111  
Met Arg Cys Leu Pro Val Leu Ile Ile Leu 10

ctg ctg ctg act gca tct gca cct ggc gtt gtt gtc cta ccg aag acc 159  
Leu Leu Leu Thr Ala Ser Ala Pro Gly Val Val Val Leu Pro Lys Thr 25

gaa gat gat gtg ccc atg tca tct gtc tac ggt aat gga aag agt atc 207  
Glu Asp Asp Val Pro Met Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile 40

cta cga gga att ctg agg aac ggt gtt tgc tgt ggc tat aag ttg tgc 255  
Leu Arg Gly Ile Leu Arg Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys 55



cat cca tgt taaccagcat gaagggaaat gactttggat gagaccctg 304  
 His Pro Cys  
 60

cgaactgtcc ctggatgtga aatttggaaa gcagactgtt cctttcgcac gtattcgtgg 364  
 aatttcgaat ggtcgtaaac aacacgctgc cacttgcagg ctactatctc tctgtccttt 424  
 catctgtgga aatggatgat ctaacaactg aaatatcaga aatttttcaa tggctataca 484  
 ctatgaccat gtagtcagta attatatcat ttggaccttt tgaaatatatt ttcaatatgt 544  
 aaagtttttg caccctggaa aggtcttttg gagttaaata ttttagtatg ttatgttttg 604  
 catacaagtt atagaatgct gtctttcttt ttgttccac atcaatgggtg ggggcagaaa 664  
 ttatttgttt tggatcaatgt aattatgacc tgcatttagt gctatagtga ttgcattttc 724  
 agcgtggaat gtttaatctg caaacagaaa gtggttgatc gactaataaa gatttgcattg 784  
 gcacaaaaaa aaaaaaaaaa agtactctgc gttgttactc gag 827

<210> 345  
 <211> 61  
 <212> PRT  
 <213> Conus marmoreus

<400> 345  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
 Ala Pro Gly Val Val Val Leu Pro Lys Thr Glu Asp Asp Val Pro Met  
 20 25 30  
 Ser Ser Val Tyr Gly Asn Gly Lys Ser Ile Leu Arg Gly Ile Leu Arg  
 35 40 45  
 Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Pro Cys  
 50 55 60

<210> 346  
 <211> 13  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 346  
 Asn Gly Val Cys Cys Gly Xaa Lys Leu Cys His Xaa Cys  
 1 5 10

<210> 347  
 <211> 12  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 347  
 Gly Val Cys Cys Gly Xaa Lys Leu Cys His Xaa Cys  
 1 5 10

<210> 348  
 <211> 202  
 <212> DNA  
 <213> Conus bandanus

<220>  
 <221> CDS  
 <222> (1)..(183)

<400> 348  
 atg cgc tgt ctc cca gtc ttg atc att ctt ctg ctg ctg act gca tct 48  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
  
 gca cct ggc gtt gat gtc cta ccg aag acc gaa gat gat gtg ccc ctg 96  
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu  
 20 25 30  
  
 tca tct gtc tac gat aat aca aag agt atc cta cga gga ctt ctg gac 144  
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp  
 35 40 45  
  
 aaa cgt gct tgc tgt ggc tac aag ctt tgc tca cca tgt taaccagcat 193  
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys  
 50 55 60  
  
 gaaggatcc 202

<210> 349  
 <211> 61  
 <212> PRT  
 <213> Conus bandanus

<400> 349  
 Met Arg Cys Leu Pro Val Leu Ile Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
  
 Ala Pro Gly Val Asp Val Leu Pro Lys Thr Glu Asp Asp Val Pro Leu  
 20 25 30  
  
 Ser Ser Val Tyr Asp Asn Thr Lys Ser Ile Leu Arg Gly Leu Leu Asp  
 35 40 45  
  
 Lys Arg Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys  
 50 55 60

<210> 350  
 <211> 11  
 <212> PRT

<213> Conus bandanus

<220>

<221> PEPTIDE

<222> (1)..(11)

<223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,  
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
O-phospho-Tyr

<400> 350

Ala Cys Cys Gly Xaa Lys Leu Cys Ser Xaa Cys  
1 5 10

<210> 351

<211> 221

<212> DNA

<213> Conus aulicus

<220>

<221> CDS

<222> (21)..(206)

<400> 351

ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu  
1 5 10

ctg ctg act gca tct gga cct agc gtt gat gcc cga ctg aag acc aaa 101  
Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys  
15 20 25

gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt acc cta 149  
Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu  
30 35 40

caa aga cat cag gac aaa agc gtt tgc tgt ggc tat aag ctg tgt ttt 197  
Gln Arg His Gln Asp Lys Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe  
45 50 55

cct tgt ggt taaccagcat gaagg 221  
Pro Cys Gly  
60

<210> 352

<211> 62

<212> PRT

<213> Conus aulicus

<400> 352

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
1 5 10 15

Gly Pro Ser Val Asp Ala Arg Leu Lys Thr Lys Asp Asp Val Pro Leu  
20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg His Gln Asp  
35 40 45

Lys Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe Pro Cys Gly  
50 55 60

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<210> 353
<211> 12
<212> PRT
<213> Conus aulicus

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr,
      125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr

<400> 353
Ser Val Cys Cys Gly Xaa Lys Leu Cys Phe Xaa Cys
1          5          10

<210> 354
<211> 312
<212> DNA
<213> Conus textile

<220>
<221> CDS
<222> (3)..(50)

<220>
<221> misc_feature
<222> (1)..(312)
<223> n is unknown

<400> 354
ca gga tcc aat ggg gtt tgt tgt ggc tat agg atg tgt gtt cct tgt      47
  Gly Ser Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys
    1          5          10          15

ggt taaccagcat gaagggaaat gactttggat gagaccctg cgaactgtcc      100
Gly

ctggatgtga gatttggaaa gcagactgtt cattttgcac gtgttcgtgg aatttcgaat      160
ggtcgttaac aacacgctgc cacttgcaag ctactatctc tctgtccttt tatctgtgga      220
actgtatgat ctaacaactg aaatatcata nanatttttc aatgggtatn cactatgcat      280
atgatcatgt agggttcaag ggggtcaagat nc      312

<210> 355
<211> 16
<212> PRT
<213> Conus textile

<400> 355
Gly Ser Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly
1          5          10          15

<210> 356
<211> 13

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<212> PRT  
 <213> Conus textile  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 7 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 356  
 Asn Gly Val Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys  
 1 5 10

<210> 357  
 <211> 205  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (1)..(186)

<400> 357  
 atg cac tgt ctc cca atc ttc gtc att ctt ctg ctg ctg act gca tct 48  
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
 gga cct agc gtt gat gcc caa ctg aag acc aaa gat gat gtg ccc ctg 96  
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu  
 20 25 30  
 tca tct ttc cga gat cat gca aag agt acc cta cga aga ctt cag gac 144  
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp  
 35 40 45  
 aaa cag act tgc tgt ggc tat agg atg tgt gtt cct tgt ggt 186  
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly  
 50 55 60  
 taaccagcat gaaggatcc 205

<210> 358  
 <211> 62  
 <212> PRT  
 <213> Conus textile

<400> 358  
 Met His Cys Leu Pro Ile Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu  
 20 25 30  
 Ser Ser Phe Arg Asp His Ala Lys Ser Thr Leu Arg Arg Leu Gln Asp  
 35 40 45  
 Lys Gln Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys Gly  
 50 55 60

<210> 359  
 <211> 12  
 <212> PRT  
 <213> Conus textile  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or hydroxy-Pro; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di--iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr  
  
 <400> 359  
 Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys  
 1 5 10  
  
 <210> 360  
 <211> 221  
 <212> DNA  
 <213> Conus ammiralis  
  
 <220>  
 <221> CDS  
 <222> (21)..(206)  
  
 <400> 360  
 agaagctgac tacaagcaga atg cac tac ctc cca gtc ttc gtc att ctt ctg 53  
 Met His Tyr Leu Pro Val Phe Val Ile Leu Leu  
 1 5 10  
  
 ctg ctg act gca tct gga cct agc gtt gat gcc caa ctg aag acc aaa 101  
 Leu Leu Thr Ala Ser Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys  
 15 20 25  
  
 gat gat gtg ccc ctg tca tct ttc cga gat aat gca aag agt acc cta 149  
 Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu  
 30 35 40  
  
 cga aga ctc cag tac aaa cag gct tgc tgt ggc ttt aag atg tgt gtt 197  
 Arg Arg Leu Gln Tyr Lys Gln Ala Cys Cys Gly Phe Lys Met Cys Val  
 45 50 55  
  
 cct tgt ggt taaccagcat gaagg 221  
 Pro Cys Gly  
 60  
  
 <210> 361  
 <211> 62  
 <212> PRT  
 <213> Conus ammiralis  
  
 <400> 361  
 Met His Tyr Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15  
  
 Gly Pro Ser Val Asp Ala Gln Leu Lys Thr Lys Asp Asp Val Pro Leu  
 20 25 30  
  
 Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Arg Arg Leu Gln Tyr  
 35 40 45

Lys Gln Ala Cys Cys Gly Phe Lys Met Cys Val Pro Cys Gly  
 50 55 60

<210> 362

<211> 12

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 11 is Pro or hydroxy-Pro

<400> 362

Xaa Ala Cys Cys Gly Phe Lys Met Cys Val Xaa Cys  
 1 5 10

<210> 363

<211> 211

<212> DNA

<213> Conus pennaceus

<220>

<221> CDS

<222> (1)..(192)

<400> 363

atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg act gca tct 48  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15

gca cct agc gtt gat gcc aaa gtt cat ctg aag acc aaa ggt gat ggg 96  
 Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly  
 20 25 30

ccc ctg tca tct ttc cga gat aat gca aag agt acc cta caa aga ctt 144  
 Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu  
 35 40 45

cag gac aaa agc act tgc tgt ggc ttt aag atg tgt att cct tgt cgt 192  
 Gln Asp Lys Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg  
 50 55 60

taaccagcat gaaggatcc 211

<210> 364

<211> 64

<212> PRT

<213> Conus pennaceus

<400> 364

Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15

Ala Pro Ser Val Asp Ala Lys Val His Leu Lys Thr Lys Gly Asp Gly  
 20 25 30

Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu





<210> 368  
 <211> 14  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Xaa at residue 12 is Pro or hydroxy-Pro; Xaa at residue 8 is Trp  
 (D or L) or bromo-Trp (D or L)

<400> 368  
 Asn Gly Val Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Asn  
 1 5 10

<210> 369  
 <211> 218  
 <212> DNA  
 <213> Conus omaria

<220>  
 <221> CDS  
 <222> (21)..(203)

<400> 369  
 ggaagctgac tacaagcaga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg 53  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu  
 1 5 10

ctg ctg act gca tct gca cct agc gtt gat gcc cga ccg aag gcc aaa 101  
 Leu Leu Thr Ala Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys  
 15 20 25

gat gat gtg ccc ctg tca tct ttc cgt gat aat gca aag agt acc cta 149  
 Asp Asp Val Pro Leu Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu  
 30 35 40

caa aga ctt cag gac aaa gac gtt tgc tgt tac gtt aga atg tgt cct 197  
 Gln Arg Leu Gln Asp Lys Asp Val Cys Cys Tyr Val Arg Met Cys Pro  
 45 50 55

tgt cgt taaccagcat gaagg 218  
 Cys Arg  
 60

<210> 370  
 <211> 61  
 <212> PRT  
 <213> Conus omaria

<400> 370  
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Thr Ala Ser  
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Ala Lys Asp Asp Val Pro Leu  
 20 25 30

Ser Ser Phe Arg Asp Asn Ala Lys Ser Thr Leu Gln Arg Leu Gln Asp  
 35 40 45

Lys Asp Val Cys Cys Tyr Val Arg Met Cys Pro Cys Arg  
 50 55 60

<210> 371  
 <211> 12  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Xaa at residue 10 is Pro or hydroxy-Pro; Xaa at residue 5 is Tyr,  
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or  
 O-phospho-Tyr

<400> 371  
 Asp Val Cys Cys Xaa Val Arg Met Cys Xaa Cys Arg  
 1 5 10

<210> 372  
 <211> 84  
 <212> PRT  
 <213> Conus radiatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(84)  
 <223> Xaa at residues 27, 32, 38, 39 and 41 is Glu or gamma-carboxy-Glu  
 ; Xaa at residues 2, 5, 17, 23, 43, 45 and 58 is Pro or hydroxy-  
 Pro; Xaa at residue 8 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-  
 Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 372  
 His Xaa Thr Lys Xaa Cys Met Xaa Cys Ser Phe Gly Gln Cys Val Gly  
 1 5 10 15

Xaa His Ile Cys Cys Gly Xaa Thr Gly Cys Xaa Met Gly Thr Ala Xaa  
 20 25 30

Ala Asn Met Cys Ser Xaa Xaa Asp Xaa Asp Xaa Ile Xaa Cys Gln Val  
 35 40 45

Phe Gly Ser Asp Cys Ala Leu Asn Asn Xaa Asp Asn Ile His Gly His  
 50 55 60

Cys Val Ala Asp Gly Ile Cys Cys Val Asp Asp Thr Cys Thr Thr His  
 65 70 75 80

Leu Gly Cys Leu

<210> 373  
 <211> 218  
 <212> DNA  
 <213> Conus tessulatus

<220>  
 <221> CDS  
 <222> (7)..(174)

<400> 373

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10

gtt tcc ttc agt gca gat cgt gcc aac gtc aaa gcg tct gac ctg atc 96  
 Val Ser Phe Ser Ala Asp Arg Ala Asn Val Lys Ala Ser Asp Leu Ile  
 15 20 25 30

gcc cag gcc acc aga gac ggc tgt cca cca cat ccc gtt cct ggc atg 144  
 Ala Gln Ala Thr Arg Asp Gly Cys Pro Pro His Pro Val Pro Gly Met  
 35 40 45

cat aag tgc atg tgt act aat aca tgt ggt tgaagacgct gatgctccag 194  
 His Lys Cys Met Cys Thr Asn Thr Cys Gly  
 50 55

gaccctctga accacgacct cgag 218

<210> 374  
 <211> 56  
 <212> PRT  
 <213> Conus tessulatus

<400> 374  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15

Phe Ser Ala Asp Arg Ala Asn Val Lys Ala Ser Asp Leu Ile Ala Gln  
 20 25 30

Ala Thr Arg Asp Gly Cys Pro Pro His Pro Val Pro Gly Met His Lys  
 35 40 45

Cys Met Cys Thr Asn Thr Cys Gly  
 50 55

<210> 375  
 <211> 20  
 <212> PRT  
 <213> Conus tessulatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(20)  
 <223> Xaa at residues 4, 5, 7 and 9 is Pro or hydroxy-Pro

<400> 375  
 Asp Gly Cys Xaa Xaa His Xaa Val Xaa Gly Met His Lys Cys Met Cys  
 1 5 10 15

Thr Asn Thr Cys  
 20

<210> 376  
 <211> 536  
 <212> DNA  
 <213> Conus geographus

<220>  
 <221> CDS

<222> (400)..(510)

<220>

<221> misc\_feature

<222> (1)..(536)

<223> n is unknown

<400> 376

anntagantn tgtcgtanta nnggatcnta antantgnnt cganatgatn angagtgata 60

aatgannggt gcactnntan ttangntnnt angatnnnna tattatnnta nnnnntaana 120

nataatnggt nnggannaaga agantaaaag tanngnttng tgaaanaang annnnatggt 180

nnanntcata acnnnaatgt aaataatana cgnnccagtg tgaaannntn tcnnnnataa 240

aaattctntn tntnaangtn nntgtntgng tgtgtgtgtg tgtgtgtgtg tgtgngtgtg 300

tgngtgtgtg tgtgtgtgtg tgtgtgtgtg nggtgtgtgn tgtgngtgtg tgtgtgtgtg 360

tgtgtgtgtg tgtgtgtgn tgtggttctg ggtccagca tct gat gnc agg gat 414

Ser Asp Xaa Arg Asp

1 5

gac aca gcc aaa gac gaa ggg tct nac atg gac aaa ttg gtc gag aaa 462

Asp Thr Ala Lys Asp Glu Gly Ser Xaa Met Asp Lys Leu Val Glu Lys

10

15

20

aaa gaa tgt tgc cat cct gcc tgt ggc aaa cac tac agt tgt gga cgc 510

Lys Glu Cys Cys His Pro Ala Cys Gly Lys His Tyr Ser Cys Gly Arg

25

30

35

tgatgctcca gggtnntgaag gancaa 536

<210> 377

<211> 37

<212> PRT

<213> Conus geographus

<220>

<221> misc\_feature

<222> (1)..(37)

<223> Xaa is unknown

<400> 377

Ser Asp Xaa Arg Asp Asp Thr Ala Lys Asp Glu Gly Ser Xaa Met Asp

1

5

10

15

Lys Leu Val Glu Lys Lys Glu Cys Cys His Pro Ala Cys Gly Lys His

20

25

30

Tyr Ser Cys Gly Arg

35

<210> 378

<211> 13

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(13)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is  
 Pro or hydroxy-Pro; Xaa at residue 11 is Tyr, 125I-Tyr, mono-  
 iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 378  
 Xaa Cys Cys His Xaa Ala Cys Gly Lys His Xaa Ser Cys  
 1 5 10

<210> 379  
 <211> 217  
 <212> DNA  
 <213> Conus geographus

<220>  
 <221> CDS  
 <222> (7)..(183)

<400> 379  
 ggatcc atg ttc acc gtg ttt ctg ttg gtg gtc ttg gca acc act gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10

gtt tcc ttc cct tca gaa cgt gca tct gat ggc agg gat gac aca gcc 96  
 Val Ser Phe Pro Ser Glu Arg Ala Ser Asp Gly Arg Asp Asp Thr Ala  
 15 20 25 30

aaa gac gaa ggg tct gac atg gag aaa ttg gtc gag aaa aaa gaa tgt 144  
 Lys Asp Glu Gly Ser Asp Met Glu Lys Leu Val Glu Lys Lys Glu Cys  
 35 40 45

tgc aat cct gcc tgt ggc aga cac ttc agt tgt gga cgc tgatgctcca 193  
 Cys Asn Pro Ala Cys Gly Arg His Phe Ser Cys Gly Arg  
 50 55

ggaccctctg aaccacgact cgag 217

<210> 380  
 <211> 59  
 <212> PRT  
 <213> Conus geographus

<400> 380  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15

Phe Pro Ser Glu Arg Ala Ser Asp Gly Arg Asp Asp Thr Ala Lys Asp  
 20 25 30

Glu Gly Ser Asp Met Glu Lys Leu Val Glu Lys Lys Glu Cys Cys Asn  
 35 40 45

Pro Ala Cys Gly Arg His Phe Ser Cys Gly Arg  
 50 55

<210> 381  
 <211> 13  
 <212> PRT  
 <213> Conus geographus

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is  
 Pro or hydroxy-Pro

<400> 381  
 Xaa Cys Cys Asn Xaa Ala Cys Gly Arg His Phe Ser Cys  
 1 5 10

<210> 382  
 <211> 224  
 <212> DNA  
 <213> Conus striatus

<220>  
 <221> CDS  
 <222> (7)..(207)

<400> 382  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10

gtt tcc ttc act tca gat cgt gca tct gat ggc agg gat gac gaa gcc 96  
 Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala  
 15 20 25 30

aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aaa gga cgc gca 144  
 Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala  
 35 40 45

tac tgt tgc cat cct gcc tgt ggc cca aac tat agt tgt ggc acc tca 192  
 Tyr Cys Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr Ser  
 50 55 60

tgc tcc agg acc ctc tgaaccacga cctcgag 224  
 Cys Ser Arg Thr Leu  
 65

<210> 383  
 <211> 67  
 <212> PRT  
 <213> Conus striatus

<400> 383  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15

Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp  
 20 25 30

Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala Tyr Cys  
 35 40 45

Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr Ser Cys Ser  
 50 55 60

Arg Thr Leu  
 65

<210> 384  
 <211> 22  
 <212> PRT  
 <213> Conus striatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residues 6 and 10 is Pro or hydroxy-Pro; Xaa at residues 2  
 and 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-  
 Tyr or O-phospho-Tyr

<400> 384  
 Ala Xaa Cys Cys His Xaa Ala Cys Gly Xaa Asn Xaa Ser Cys Gly Thr  
 1 5 10 15  
 Ser Cys Ser Arg Thr Leu  
 20

<210> 385  
 <211> 224  
 <212> DNA  
 <213> Conus striatus

<220>  
 <221> CDS  
 <222> (7)..(189)

<400> 385  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10  
 gtt tcc ttc act tca gat cgt gca tct gat ggc agg gat gac gaa gcc 96  
 Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala  
 15 20 25 30  
 aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aaa gga cgc gca 144  
 Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala  
 35 40 45  
 tac tgt tgc cat cct gtc tgt ggc aaa aac ttt gat tgt gga cgc 189  
 Tyr Cys Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys Gly Arg  
 50 55 60  
 tgatgctcca ggaccctctg aaccacgacc tcgag 224

<210> 386  
 <211> 61  
 <212> PRT  
 <213> Conus striatus

<400> 386  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp  
 20 25 30

Glu Arg Ser Asp Met His Glu Ser Asp Arg Lys Gly Arg Ala Tyr Cys  
35 40 45

Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys Gly Arg  
50 55 60

```
<210> 387
<211> 14
<212> PRT
<213> Conus striatus
```

```
<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 6 is Pro or hydroxy-Pro; Xaa at residue 2 is Tyr,
125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
O-phospho-Tyr
```

<400> 387  
Ala Xaa Cys Cys His Xaa Val Cys Gly Lys Asn Phe Asp Cys  
1 5 10

```
<210> 388
<211> 224
<212> DNA
<213> Conus rattus
```

```
<220>
<221> CDS
<222> (7) .. (207)
```

```

<400> 388
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
      Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
      1             5             10

```

ggt tcc ttc cct tca gat cgt gca tct gat ggc agg gat gac gaa gcc 96  
Val Ser Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala  
15 20 25 30

aaa gac gaa agg tct gac atg cac gaa tcg gac cgg aat gga cgc gga 144  
Lys Asp Glu Arg Ser Asp Met His Glu Ser Asp Arg Asn Gly Arg Gly  
35 40 45

tgc tgt tgc aat cct gcc tgt ggc cca aac tat ggt tgt ggc acc tca 192  
Cys Cys Cys Asn Pro Ala Cys Gly Pro Asn Tyr Gly Cys Gly Thr Ser  
50 55 60

tgc tcc agg acc ctc tgaaccacga cctcgag 224  
Cys Ser Arg Thr Leu  
65

```
<210> 389
<211> 67
<212> PRT
<213> Conus rattus
```

```
<400> 389
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1          5          10          15
```



Phe Pro Ser Asp Arg Ala Ser Asp Gly Arg Asp Asp Glu Ala Lys Asp  
20 25 30

Glu Arg Ser Asp Met His Glu Ser Asp Arg Asn Gly Arg Gly Cys Cys  
35 40 45

Cys Asn Pro Ala Cys Gly Pro Asn Tyr Gly Cys Gly Thr Ser Cys Ser  
50 55 60

Arg Thr Leu  
65

<210> 390

<211> 22

<212> PRT

<213> Conus rattus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residues 6 and 10 is Pro or hydroxy-Pro; Xaa at residue  
12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
or O-phospho-Tyr

<400> 390

Gly Cys Cys Cys Asn Xaa Ala Cys Gly Xaa Asn Xaa Gly Cys Gly Thr  
1 5 10 15

Ser Cys Ser Arg Thr Leu  
20

<210> 391

<211> 230

<212> DNA

<213> Conus arenatus

<220>

<221> CDS

<222> (7)..(195)

<400> 391

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg 48  
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
1 5 10

gat tcc ttc act cca gtt cgt act tct gtt ggc agg agt gct gca gcc 96  
Asp Ser Phe Thr Pro Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala  
15 20 25 30

aac gcg ttt gac cgg atc gct ctg acc gcc agg caa gat tat tgc tgt 144  
Asn Ala Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys  
35 40 45

acc att ccc agc tgt tgg gat cgc tat aaa gag aga tgt aga cac ata 192  
Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile  
50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc ttgag 230  
Arg

<210> 392  
 <211> 63  
 <212> PRT  
 <213> Conus arenatus

<400> 392  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Asp Ser  
 1 5 10 15  
 Phe Thr Pro Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala Asn Ala  
 20 25 30  
 Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys Thr Ile  
 35 40 45  
 Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile Arg  
 50 55 60

<210> 393  
 <211> 22  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 16 is Glu or  
 gamma-carboxy-Glu; Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at  
 residue 11 is Trp (D or L) or bromo-Trp (D or L);

<220>  
 <221> PEPTIDE  
 <222> (1)..(22)  
 <223> Xaa at residues 3 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-  
 -Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 393  
 Xaa Asp Xaa Cys Cys Thr Ile Xaa Ser Cys Xaa Asp Arg Xaa Lys Xaa  
 1 5 10 15  
 Arg Cys Arg His Ile Arg  
 20

<210> 394  
 <211> 230  
 <212> DNA  
 <213> Conus eburneus

<220>  
 <221> CDS  
 <222> (7)..(195)

<400> 394  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtg 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10  
 gat tcc ttc act tca gtt cgt act tcc gtt ggc agg agt gct gca gcc 96  
 Asp Ser Phe Thr Ser Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala

```

15              20              25              30
aac gcg ttt gac cgg atc gct ctg acc gcc agg caa gat tat tgc tgt      144
Asn Ala Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys
              35              40              45

acc att ccc agc tgt tgg gat cgc tat aaa gag aga tgt aga cac ata      192
Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile
              50              55              60

cgc tgatgctcca ggaccctctg aaccacgacc tcgag      230
Arg

```

```

<210> 395
<211> 63
<212> PRT
<213> Conus eburneus

```

```

<400> 395
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Asp Ser
1              5              10              15

Phe Thr Ser Val Arg Thr Ser Val Gly Arg Ser Ala Ala Ala Asn Ala
              20              25              30

Phe Asp Arg Ile Ala Leu Thr Ala Arg Gln Asp Tyr Cys Cys Thr Ile
              35              40              45

Pro Ser Cys Trp Asp Arg Tyr Lys Glu Arg Cys Arg His Ile Arg
              50              55              60

```

```

<210> 396
<211> 22
<212> PRT
<213> Conus eburneus

```

```

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residue 16 is Glu or
gamma-carboxy-Glu; Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at
residue 11 is Trp (D or L) or bromo-Trp (D or L);

```

```

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residues 3 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo
-Tyr, O-sulpho-Tyr or O-phospho-Tyr

```

```

<400> 396
Xaa Asp Xaa Cys Cys Thr Ile Xaa Ser Cys Xaa Asp Arg Xaa Lys Xaa
1              5              10              15

Arg Cys Arg His Ile Arg
              20

```

```

<210> 397
<211> 221
<212> DNA
<213> Conus miles

```

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(177)

&lt;400&gt; 397

```

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act gct gtt      48
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val
1           5           10

```

```

ctt cca gtc act tta gat cgt gca tct gat gga agg aat gca gca gcc      96
Leu Pro Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala
15           20           25           30

```

```

aac gcc aaa acg cct cgc ctg atc gcg cca ttc atc agg gat tat tgc      144
Asn Ala Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys
           35           40           45

```

```

tgt cat aga ggt ccc tgt atg gta tgg tgt ggt tgaagccgct gctgctccag    197
Cys His Arg Gly Pro Cys Met Val Trp Cys Gly
           50           55

```

```

gaccctctga accacgacct cgag                                          221

```

&lt;210&gt; 398

&lt;211&gt; 57

&lt;212&gt; PRT

&lt;213&gt; Conus miles

&lt;400&gt; 398

```

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Ala Val Leu Pro
1           5           10           15

```

```

Val Thr Leu Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Asn Ala
           20           25           30

```

```

Lys Thr Pro Arg Leu Ile Ala Pro Phe Ile Arg Asp Tyr Cys Cys His
           35           40           45

```

```

Arg Gly Pro Cys Met Val Trp Cys Gly
           50           55

```

&lt;210&gt; 399

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Conus miles

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(13)

```

<223> Xaa at residue 8 is Pro or hydroxy-Pro; Xaa at residue 12 is Trp
      (D or L) or bromo-Trp (D or L); Xaa at residue 2 is Tyr, 125I-Tyr
      , mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

```

&lt;400&gt; 399

```

Asp Xaa Cys Cys His Arg Gly Xaa Cys Met Val Xaa Cys
1           5           10

```

&lt;210&gt; 400

&lt;211&gt; 218

```

<212> DNA
<213> Conus jDedius

<220>
<221> CDS
<222> (7)..(174)

<400> 400
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc      48
      Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
        1             5             10

      gtt tcc aac tct tca gat cgt ggt cca gca tct aat aaa agg aag aat      96
      Val Ser Asn Ser Ser Asp Arg Gly Pro Ala Ser Asn Lys Arg Lys Asn
      15             20             25             30

      gcc gca atg ctt gac atg atc gct caa cac gcc ata agg ggt tgc tgt      144
      Ala Ala Met Leu Asp Met Ile Ala Gln His Ala Ile Arg Gly Cys Cys
              35             40             45

      tcc gat cct cgc tgt aga tat aga tgt cgt tgaagacgct gctgctccag      194
      Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg
              50             55

      gaccctctga accacgacct cgag      218

<210> 401
<211> 56
<212> PRT
<213> Conus jDedius

<400> 401
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1             5             10             15
Asn Ser Ser Asp Arg Gly Pro Ala Ser Asn Lys Arg Lys Asn Ala Ala
      20             25             30

Met Leu Asp Met Ile Ala Gln His Ala Ile Arg Gly Cys Cys Ser Asp
      35             40             45

Pro Arg Cys Arg Tyr Arg Cys Arg
      50             55

<210> 402
<211> 13
<212> PRT
<213> Conus jDedius

<220>
<221> PEPTIDE
<222> (1)..(13)
<223> Xaa at residue 6 is Pro or hydroxy-Pro;Xaa at residue 10 is Tyr,
      125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr

<400> 402
Gly Cys Cys Ser Asp Xaa Arg Cys Arg Xaa Arg Cys Arg
1             5             10

<210> 403

```

<211> 17  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro

<400> 403  
 Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys  
 1 5 10 15

Gly

<210> 404  
 <211> 17  
 <212> PRT  
 <213> Conus omaria

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residues 6 and 13 is Pro or hydroxy-Pro; C terminus contains free hydroxyl

<400> 404  
 Gly Cys Cys Ser His Xaa Ala Cys Asn Val Asn Asn Xaa His Ile Cys  
 1 5 10 15

Gly

<210> 405  
 <211> 224  
 <212> DNA  
 <213> Conus quercinus

<220>  
 <221> CDS  
 <222> (7)..(189)

<400> 405  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10

act tca gat cgt gta tct aat ggc agg aaa gct gca gcc aaa ttc aaa 96  
 Thr Ser Asp Arg Val Ser Asn Gly Arg Lys Ala Ala Ala Lys Phe Lys  
 15 20 25 30

gcg cct gcc ctg atg gag ctg tcc gtc agg caa gga tgc tgt tca gat 144  
 Ala Pro Ala Leu Met Glu Leu Ser Val Arg Gln Gly Cys Cys Ser Asp  
 35 40 45

cct gcc tgt gcc gtg agc aat cca gac atc tgt ggc gga gga cgc 189  
 Pro Ala Cys Ala Val Ser Asn Pro Asp Ile Cys Gly Gly Gly Arg  
 50 55 60

tgatgctcca ggaccctctg aaccacgacc tcgag 224

<210> 406  
 <211> 61  
 <212> PRT  
 <213> Conus quercinus

<400> 406  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Thr Ser  
 1 5 10 15  
 Asp Arg Val Ser Asn Gly Arg Lys Ala Ala Ala Lys Phe Lys Ala Pro  
 20 25 30  
 Ala Leu Met Glu Leu Ser Val Arg Gln Gly Cys Cys Ser Asp Pro Ala  
 35 40 45  
 Cys Ala Val Ser Asn Pro Asp Ile Cys Gly Gly Gly Arg  
 50 55 60

<210> 407  
 <211> 19  
 <212> PRT  
 <213> Conus quercinus

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Xaa at residue 1 is Gln or pyro-Gln; Xaa at residues 7 and 14 is  
 Pro or hydroxy-Pro

<400> 407  
 Xaa Gly Cys Cys Ser Asp Xaa Ala Cys Ala Val Ser Asn Xaa Asp Ile  
 1 5 10 15

Cys Gly Gly

<210> 408  
 <211> 230  
 <212> DNA  
 <213> Conus bandanus

<220>  
 <221> CDS  
 <222> (7)..(186)

<400> 408  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10  
 gtt tcc ttc act tca aat cgt gca ttt cgt cgt agg aat gcc gta gcc 96  
 Val Ser Phe Thr Ser Asn Arg Ala Phe Arg Arg Arg Asn Ala Val Ala  
 15 20 25 30  
 aaa gcg tct gac ctg atc gct ctg aac gcc agg aga cca gaa tgc tgt 144  
 Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu Cys Cys  
 35 40 45  
 act cat cct gcc tgt cac gtg agt cat cca gaa ctc tgt ggt 186  
 Thr His Pro Ala Cys His Val Ser His Pro Glu Leu Cys Gly  
 50 55 60

tgaagacgct gacgctccag gaccctctga accacgacct cgag

230

<210> 409

<211> 60

<212> PRT

<213> Conus bandanus

<400> 409

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
1 5 10 15

Phe Thr Ser Asn Arg Ala Phe Arg Arg Arg Asn Ala Val Ala Lys Ala  
20 25 30

Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu Cys Cys Thr His  
35 40 45

Pro Ala Cys His Val Ser His Pro Glu Leu Cys Gly  
50 55 60

<210> 410

<211> 17

<212> PRT

<213> Conus bandanus

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at  
residues 1, 7 and 14 is Pro or hydroxy-Pro

<400> 410

Xaa Xaa Cys Cys Thr His Xaa Ala Cys His Val Ser His Xaa Xaa Leu  
1 5 10 15

Cys

<210> 411

<211> 242

<212> DNA

<213> Conus marmoreus

<220>

<221> CDS

<222> (7)..(198)

<400> 411

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48  
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
1 5 10

gtt tcc ttc act tca aat cgt gtt ctg gat cca gca ttt cgt cgt agg 96  
Val Ser Phe Thr Ser Asn Arg Val Leu Asp Pro Ala Phe Arg Arg Arg  
15 20 25 30

aat gcc gca gcc aaa gcg tct gac ctg atc gct ctg aac gcc agg aga 144  
Asn Ala Ala Ala Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg  
35 40 45



cca gaa tgc tgt act cat cct gcc tgt cac gtg agt aat cca gaa ctc 192  
Pro Glu Cys Cys Thr His Pro Ala Cys His Val Ser Asn Pro Glu Leu  
50 55 60

tgt ggc tgaagacgct gatgctccag gaccctctga accacgacct cgag 242  
Cys Gly

```
<210> 412
<211> 64
<212> PRT
<213> Conus marmoreus
```

```
<400> 412
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser
1          5          10          15
```

Phe Thr Ser Asn Arg Val Leu Asp Pro Ala Phe Arg Arg Arg Asn Ala  
20 25 30

Ala Ala Lys Ala Ser Asp Leu Ile Ala Leu Asn Ala Arg Arg Pro Glu  
35 40 45

Cys Cys Thr His Pro Ala Cys His Val Ser Asn Pro Glu Leu Cys Gly  
50 55 60

```
<210> 413
<211> 17
<212> PRT
<213> Conus marmoreus
```

```
<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residues 2 and 15 is Glu or gamma-carboxy-Glu; Xaa at
residues 1, 7 and 14 is Pro or hydroxy-Pro
```

```
<400> 413
Xaa Xaa Cys Cys Thr His Xaa Ala Cys His Val Ser Asn Xaa Xaa Leu
1          5          10          15
```

Cys

```
<210> 414
<211> 218
<212> DNA
<213> Conus miles
```

```
<220>
<221> CDS
<222> (7) .. (174)
```

```

<400> 414
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48
      Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val
      1             5             10

```

ggt tcc gtc act tca tat cgt gca tct cat ggc agg aag gac gca gcc 96  
Val Ser Val Thr Ser Tyr Arg Ala Ser His Gly Arg Lys Asp Ala Ala  
15 20 25 30

gac ctg agc gct ctg aac gac aac aat aat tgc tgt aac cat cct gcc 144  
 Asp Leu Ser Ala Leu Asn Asp Asn Asn Asn Cys Cys Asn His Pro Ala  
                   35                                  40                                  45

tgt gcc ggg aaa aat tca gat ctt tgt ggt tgaagacgct gctgctccag 194  
 Cys Ala Gly Lys Asn Ser Asp Leu Cys Gly  
                   50                                  55

gaccctctga accacgacct cgag 218

<210> 415  
 <211> 56  
 <212> PRT  
 <213> Conus miles

<400> 415  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1                  5                                  10                                  15

Val Thr Ser Tyr Arg Ala Ser His Gly Arg Lys Asp Ala Ala Asp Leu  
                   20                                  25                                  30

Ser Ala Leu Asn Asp Asn Asn Asn Cys Cys Asn His Pro Ala Cys Ala  
                   35                                  40                                  45

Gly Lys Asn Ser Asp Leu Cys Gly  
           50                                  55

<210> 416  
 <211> 15  
 <212> PRT  
 <213> Conus miles

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residue 5 is Pro or hydroxy-Pro

<400> 416  
 Cys Cys Asn His Xaa Ala Cys Ala Gly Lys Asn Ser Asp Leu Cys  
 1                  5                                  10                                  15

<210> 417  
 <211> 16  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residue 11 is Glu or gamma-carboxy-Glu; Xaa at residue 6  
       is Pro or hydroxy-Pro; Xaa at residue 4 is Tyr, 125I-Tyr, mono-  
       iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 417  
 Gly Cys Cys Xaa His Xaa Thr Cys His Leu Xaa His Ser Asn Leu Cys  
 1                  5                                  10                                  15

<210> 418  
 <211> 224

<212> DNA  
<213> *Conus nobilis*

<220>  
<221> CDS  
<222> (7)..(189)

<220>  
<221> misc\_feature  
<222> (1)..(224)  
<223> n is unknown

<400> 418  
ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtt 48  
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
1 5 10  
  
gtt tcc ttc act tca gat cgt gca tct gat ggc agg aat gcc gca gcc 96  
Val Ser Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala  
15 20 25 30  
  
aaa gct tct gac ctg att gct ttg acc gtc agg gga tgc tgt gag cga 144  
Lys Ala Ser Asp Leu Ile Ala Leu Thr Val Arg Gly Cys Cys Glu Arg  
35 40 45  
  
cct ccc tgt cgc tgg caa aat cca gat ctt tgt ggt gga agg cgc 189  
Pro Pro Cys Arg Trp Gln Asn Pro Asp Leu Cys Gly Gly Arg Arg  
50 55 60  
  
tganattcca ggaccctctg aaccacgacc tcgag 224

<210> 419  
<211> 61  
<212> PRT  
<213> *Conus nobilis*

<400> 419  
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
1 5 10 15  
  
Phe Thr Ser Asp Arg Ala Ser Asp Gly Arg Asn Ala Ala Ala Lys Ala  
20 25 30  
  
Ser Asp Leu Ile Ala Leu Thr Val Arg Gly Cys Cys Glu Arg Pro Pro  
35 40 45  
  
Cys Arg Trp Gln Asn Pro Asp Leu Cys Gly Gly Arg Arg  
50 55 60

<210> 420  
<211> 17  
<212> PRT  
<213> *Conus nobilis*

<220>  
<221> PEPTIDE  
<222> (1)..(17)  
<223> Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residues 6,  
7 and 13 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L)  
or bromo-Trp (D or L)

&lt;400&gt; 420

Gly Cys Cys Xaa Arg Xaa Xaa Cys Arg Xaa Gln Asn Xaa Asp Leu Cys  
 1 5 10 15

Gly

&lt;210&gt; 421

&lt;211&gt; 233

&lt;212&gt; DNA

<213> *Conus atlanticus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(198)

&lt;400&gt; 421

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc aca gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10

gtt tcc ttc act tca gat agt gca ttt gat agc agg aat gtc gca gcc 96  
 Val Ser Phe Thr Ser Asp Ser Ala Phe Asp Ser Arg Asn Val Ala Ala  
 15 20 25 30

aac gac aaa gtg tct gac atg atc gct ctg acc gcc agg aga aca tgc 144  
 Asn Asp Lys Val Ser Asp Met Ile Ala Leu Thr Ala Arg Arg Thr Cys  
 35 40 45

tgt tcc cgt cct acc tgt aga atg gaa tat cca gaa ctt tgt ggt gga 192  
 Cys Ser Arg Pro Thr Cys Arg Met Glu Tyr Pro Glu Leu Cys Gly Gly  
 50 55 60

aga cgc tgatactcca ggacctctg aaccacgacc tcgag 233  
 Arg Arg

&lt;210&gt; 422

&lt;211&gt; 64

&lt;212&gt; PRT

<213> *Conus atlanticus*

&lt;400&gt; 422

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15

Phe Thr Ser Asp Ser Ala Phe Asp Ser Arg Asn Val Ala Ala Asn Asp  
 20 25 30

Lys Val Ser Asp Met Ile Ala Leu Thr Ala Arg Arg Thr Cys Cys Ser  
 35 40 45

Arg Pro Thr Cys Arg Met Glu Tyr Pro Glu Leu Cys Gly Gly Arg Arg  
 50 55 60

&lt;210&gt; 423

&lt;211&gt; 17

&lt;212&gt; PRT

<213> *Conus atlanticus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residues 11 and 14 is Glu or gamma-carboxy-Glu; Xaa at residues 6 and 13 is Pro or hydroxy-Pro; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr

<400> 423  
 Thr Cys Cys Ser Arg Xaa Thr Cys Arg Met Xaa Xaa Xaa Xaa Leu Cys  
 1 5 10 15

Gly

<210> 424  
 <211> 227  
 <212> DNA  
 <213> Conus quercinus

<220>  
 <221> CDS  
 <222> (7)..(192)

<220>  
 <221> misc\_feature  
 <222> (1)..(227)  
 <223> n is unknown

<400> 424  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca atc acg gtg 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val  
 1 5 10

gtt tcc ttc acc tca gat cat gca tct gat ggc agg aat acc gca gcc 96  
 Val Ser Phe Thr Ser Asp His Ala Ser Asp Gly Arg Asn Thr Ala Ala  
 15 20 25 30

aac gac aaa gcg tct aaa ctg atg gct ctt acg aac gaa tgc tgt gac 144  
 Asn Asp Lys Ala Ser Lys Leu Met Ala Leu Thr Asn Glu Cys Cys Asp  
 35 40 45

aat cct ccg tgc aag tcg agt aat cca gat ttg tgt gac tgg aga agc 192  
 Asn Pro Pro Cys Lys Ser Ser Asn Pro Asp Leu Cys Asp Trp Arg Ser  
 50 55 60

tgatgctcca ggaccctntg aaccacgacc tcgag 227

<210> 425  
 <211> 62  
 <212> PRT  
 <213> Conus quercinus

<400> 425  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Ile Thr Val Val Ser  
 1 5 10 15

Phe Thr Ser Asp His Ala Ser Asp Gly Arg Asn Thr Ala Ala Asn Asp  
 20 25 30

Lys Ala Ser Lys Leu Met Ala Leu Thr Asn Glu Cys Cys Asp Asn Pro  
                   35                                  40                                  45

Pro Cys Lys Ser Ser Asn Pro Asp Leu Cys Asp Trp Arg Ser  
           50                                  55                                  60

<210> 426

<211> 21

<212> PRT

<213> Conus quercinus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 2 is Glu or gamma-carboxy-Glu; Xaa at residues 7,  
       8 and 14 is Pro or hydroxy-Pro; Xaa at residue 19 is Trp (D or L)  
       or bromo-Trp (D or L)

<400> 426

Asn Xaa Cys Cys Asp Asn Xaa Xaa Cys Lys Ser Ser Asn Xaa Asp Leu  
   1                                  5                                  10                                  15

Cys Asp Xaa Arg Ser  
                   20

<210> 427

<211> 221

<212> DNA

<213> Conus leopardus

<220>

<221> CDS

<222> (7)..(177)

<400> 427

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acg gtc 48  
           Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
           1                                  5                                  10

gtt tcc ctc act tta gat cgt gca tct ggt ggc agg aga tct gga gcc 96  
   Val Ser Leu Thr Leu Asp Arg Ala Ser Gly Gly Arg Arg Ser Gly Ala  
   15                                  20                                  25                                  30

gac aac atg att gct ctt ctg atc atc aga aaa tgc tgt tcc aat ccc 144  
   Asp Asn Met Ile Ala Leu Leu Ile Ile Arg Lys Cys Cys Ser Asn Pro  
                                   35                                  40                                  45

gcc tgt aac agg tat aat cca gca att tgt gat tgaagacgct aatgctccag 197  
   Ala Cys Asn Arg Tyr Asn Pro Ala Ile Cys Asp  
                                   50                                  55

gaccctctga accacgacct cgag 221

<210> 428

<211> 57

<212> PRT

<213> Conus leopardus

<400> 428

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser

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1              5              10              15
Leu Thr Leu Asp Arg Ala Ser Gly Gly Arg Arg Ser Gly Ala Asp Asn
      20              25              30

Met Ile Ala Leu Leu Ile Ile Arg Lys Cys Cys Ser Asn Pro Ala Cys
      35              40              45

Asn Arg Tyr Asn Pro Ala Ile Cys Asp
      50              55

<210> 429
<211> 16
<212> PRT
<213> Conus leopardus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residues 5 and 12 is Pro or hydroxy-Pro; Xaa at residue 10
      is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
      O-phospho-Tyr

<400> 429
Cys Cys Ser Asn Xaa Ala Cys Asn Arg Xaa Asn Xaa Ala Ile Cys Asp
1              5              10              , 15

<210> 430
<211> 224
<212> DNA
<213> Conus emaciatus

<220>
<221> CDS
<222> (7)..(180)

<400> 430
ggatcc atg ttc acc gtg ttt ctg ttg gtt ctc ttg gca acc act gtc      48
      Met Phe Thr Val Phe Leu Leu Val Leu Leu Ala Thr Thr Val
      1              5              10

act tta cat cgt gca tct aat ggc agg aat gcc gca gcc agc agg aaa      96
Thr Leu His Arg Ala Ser Asn Gly Arg Asn Ala Ala Ala Ser Arg Lys
15              20              25              30

gcg tct gcc ctg atc gct cag atc gcc ggt aga gac tgc tgt aac ttt      144
Ala Ser Ala Leu Ile Ala Gln Ile Ala Gly Arg Asp Cys Cys Asn Phe
      35              40              45

cct gct tgt gcc gcg agt aat cca ggc ctt tgt act tgaagacgct      190
Pro Ala Cys Ala Ala Ser Asn Pro Gly Leu Cys Thr
      50              55

gtgtgtccag gacctctga accacgacct cgag      224

<210> 431
<211> 58
<212> PRT
<213> Conus emaciatus

```

&lt;400&gt; 431

Met Phe Thr Val Phe Leu Leu Val Leu Leu Ala Thr Thr Val Thr Leu  
 1 5 10 15

His Arg Ala Ser Asn Gly Arg Asn Ala Ala Ala Ser Arg Lys Ala Ser  
 20 25 30

Ala Leu Ile Ala Gln Ile Ala Gly Arg Asp Cys Cys Asn Phe Pro Ala  
 35 40 45

Cys Ala Ala Ser Asn Pro Gly Leu Cys Thr  
 50 55

&lt;210&gt; 432

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus emaciatus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(17)

&lt;223&gt; Xaa at residues 6 and 13 is Pro or hydroxy-Pro

&lt;400&gt; 432

Asp Cys Cys Asn Phe Xaa Ala Cys Ala Ala Ser Asn Xaa Gly Leu Cys  
 1 5 10 15

Thr

&lt;210&gt; 433

&lt;211&gt; 215

&lt;212&gt; DNA

&lt;213&gt; Conus victor

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(180)

&lt;400&gt; 433

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc acc atc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile  
 1 5 10

gtt tcc tcc act tta gat cgt gca tct gat ggc atg aat gct gca gcg 96  
 Val Ser Ser Thr Leu Asp Arg Ala Ser Asp Gly Met Asn Ala Ala Ala  
 15 20 25 30

tct gac ctg atc gct ctg agc atc agg aga tgc tgt tct tct cct ccc 144  
 Ser Asp Leu Ile Ala Leu Ser Ile Arg Arg Cys Cys Ser Ser Pro Pro  
 35 40 45

tgt ttc gcg agt aat cca gct tgt ggt aga cga cgc tgatgctcca 190  
 Cys Phe Ala Ser Asn Pro Ala Cys Gly Arg Arg Arg  
 50 55

ggaccctctg aaccacgacc tcgag 215

&lt;210&gt; 434

&lt;211&gt; 58

&lt;212&gt; PRT



<213> Conus victor

<400> 434

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile Val Ser  
1 5 10 15

Ser Thr Leu Asp Arg Ala Ser Asp Gly Met Asn Ala Ala Ala Ser Asp  
20 25 30

Leu Ile Ala Leu Ser Ile Arg Arg Cys Cys Ser Ser Pro Pro Cys Phe  
35 40 45

Ala Ser Asn Pro Ala Cys Gly Arg Arg Arg  
50 55

<210> 435

<211> 14

<212> PRT

<213> Conus victor

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residues 5, 6 and 13 is Pro or hydroxy-Pro

<400> 435

Cys Cys Ser Ser Xaa Xaa Cys Phe Ala Ser Asn Xaa Ala Cys  
1 5 10

<210> 436

<211> 230

<212> DNA

<213> Conus cinereus gubba

<220>

<221> CDS

<222> (7)..(195)

<400> 436

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ctg gca acc act atc 48  
Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile  
1 5 10

ggt tcc tcc act tca ggt cat gca ttt gat ggc agg aat gct gca gcc 96  
Val Ser Ser Thr Ser Gly His Ala Phe Asp Gly Arg Asn Ala Ala Ala  
15 20 25 30

gac tac aaa ggg tct gaa ttg ctt gct atg acc gtc agg gga gga tgc 144  
Asp Tyr Lys Gly Ser Glu Leu Leu Ala Met Thr Val Arg Gly Gly Cys  
35 40 45

tgt tcc ttt cct ccc tgt atc gca aat aat cct ttt tgt gct gga aga 192  
Cys Ser Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys Ala Gly Arg  
50 55 60

cgc tgatgctcca ggaccctctg aaccacgacc tcgag 230  
Arg

<210> 437

<211> 63

&lt;212&gt; PRT

&lt;213&gt; Conus cinereus gubba

&lt;400&gt; 437

Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Ile Val Ser  
 1 5 10 15

Ser Thr Ser Gly His Ala Phe Asp Gly Arg Asn Ala Ala Ala Asp Tyr  
 20 25 30

Lys Gly Ser Glu Leu Leu Ala Met Thr Val Arg Gly Gly Cys Cys Ser  
 35 40 45

Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys Ala Gly Arg Arg  
 50 55 60

&lt;210&gt; 438

&lt;211&gt; 17

&lt;212&gt; PRT

&lt;213&gt; Conus cinereus gubba

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(17)

&lt;223&gt; Xaa at residues 7, 8 and 14 is Pro or hydroxy-Pro

&lt;400&gt; 438

Gly Gly Cys Cys Ser Phe Xaa Xaa Cys Ile Ala Asn Asn Xaa Phe Cys  
 1 5 10 15

Ala

&lt;210&gt; 439

&lt;211&gt; 221

&lt;212&gt; DNA

&lt;213&gt; Conus flavidus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (7)..(177)

&lt;400&gt; 439

ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val  
 1 5 10

act tta gat cgt gca tct cat ggc agg tat atc cca gtc gtc gac aga 96  
 Thr Leu Asp Arg Ala Ser His Gly Arg Tyr Ile Pro Val Val Asp Arg  
 15 20 25 30

gcg tct gcc ctg atg gct cag gcc gac ctt aga ggt tgc tgt tcc aat 144  
 Ala Ser Ala Leu Met Ala Gln Ala Asp Leu Arg Gly Cys Cys Ser Asn  
 35 40 45

cct cct tgt tcc tat ctt aat cca gcc tgt ggt taaagacgct gccgctccag 197  
 Pro Pro Cys Ser Tyr Leu Asn Pro Ala Cys Gly  
 50 55

gaccctctga accacgacct cgag 221

<210> 440  
 <211> 57  
 <212> PRT  
 <213> Conus flavidus

<400> 440  
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu  
 1 5 10 15  
 Asp Arg Ala Ser His Gly Arg Tyr Ile Pro Val Val Asp Arg Ala Ser  
 20 25 30  
 Ala Leu Met Ala Gln Ala Asp Leu Arg Gly Cys Cys Ser Asn Pro Pro  
 35 40 45  
 Cys Ser Tyr Leu Asn Pro Ala Cys Gly  
 50 55

<210> 441  
 <211> 15  
 <212> PRT  
 <213> Conus flavidus

<220>  
 <221> PEPTIDE  
 <222> (1)..(15)  
 <223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro; Xaa at residue  
 10 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 441  
 Gly Cys Cys Ser Asn Xaa Xaa Cys Ser Xaa Leu Asn Xaa Ala Cys  
 1 5 10 15

<210> 442  
 <211> 221  
 <212> DNA  
 <213> Conus emaciatus

<220>  
 <221> CDS  
 <222> (7)..(177)

<400> 442  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttc gca tcc tct gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val  
 1 5 10  
 act tta gat cgt gca tct cat ggc agg tat gcc gca gtc gtc aac aga 96  
 Thr Leu Asp Arg Ala Ser His Gly Arg Tyr Ala Ala Val Val Asn Arg  
 15 20 25 30  
 gcg tct gcc ctg atg gct cat gcc gcc ctt cga gat tgc tgt tcc gat 144  
 Ala Ser Ala Leu Met Ala His Ala Ala Leu Arg Asp Cys Cys Ser Asp  
 35 40 45  
 cct cct tgt gct cat aat aat cca gac tgt cgt taaagacgct gctgctccag 197  
 Pro Pro Cys Ala His Asn Asn Pro Asp Cys Arg  
 50 55  
 gaccctctga accacgacct cgag 221

<210> 443  
 <211> 57  
 <212> PRT  
 <213> Conus emaciatus

<400> 443  
 Met Phe Thr Val Phe Leu Leu Val Val Phe Ala Ser Ser Val Thr Leu  
 1 5 10 15  
 Asp Arg Ala Ser His Gly Arg Tyr Ala Ala Val Val Asn Arg Ala Ser  
 20 25 30  
 Ala Leu Met Ala His Ala Ala Leu Arg Asp Cys Cys Ser Asp Pro Pro  
 35 40 45  
 Cys Ala His Asn Asn Pro Asp Cys Arg  
 50 55

<210> 444  
 <211> 16  
 <212> PRT  
 <213> Conus emaciatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(16)  
 <223> Xaa at residues 6, 7 and 13 is Pro or hydroxy-Pro

<400> 444  
 Asp Cys Cys Ser Asp Xaa Xaa Cys Ala His Asn Asn Xaa Asp Cys Arg  
 1 5 10 15

<210> 445  
 <211> 230  
 <212> DNA  
 <213> Conus generalis

<220>  
 <221> CDS  
 <222> (7)..(195)

<400> 445  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca act act gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10  
 gtt tcc ttc act tca gat cgt ggg tct gat ggc agg aat gcc gca gcc 96  
 Val Ser Phe Thr Ser Asp Arg Gly Ser Asp Gly Arg Asn Ala Ala Ala  
 15 20 25 30  
 aag gac aaa gcg tct gac ctg gtc gct ctg acc gtc aag gga tgc tgt 144  
 Lys Asp Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys  
 35 40 45  
 tct aat cct ccc tgt tac gcg aat aat caa gcc tat tgt aat gga aga 192  
 Ser Asn Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys Asn Gly Arg  
 50 55 60  
 cgc tgatgctcca ggaccctctg aaccacgacc tcgag 230

Arg

<210> 446  
 <211> 63  
 <212> PRT  
 <213> Conus generalis

<400> 446  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 Phe Thr Ser Asp Arg Gly Ser Asp Gly Arg Asn Ala Ala Ala Lys Asp  
 20 25 30  
 Lys Ala Ser Asp Leu Val Ala Leu Thr Val Lys Gly Cys Cys Ser Asn  
 35 40 45  
 Pro Pro Cys Tyr Ala Asn Asn Gln Ala Tyr Cys Asn Gly Arg Arg  
 50 55 60

<210> 447  
 <211> 17  
 <212> PRT  
 <213> Conus generalis

<220>  
 <221> PEPTIDE  
 <222> (1)..(17)  
 <223> Xaa at residues 6 and 7 is Pro or hydroxy-Pro; Xaa at residues 9  
 and 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 447  
 Gly Cys Cys Ser Asn Xaa Xaa Cys Xaa Ala Asn Asn Gln Ala Xaa Cys  
 1 5 10 15

Asn

<210> 448  
 <211> 212  
 <212> DNA  
 <213> Conus wittigi

<220>  
 <221> CDS  
 <222> (7)..(195)

<400> 448  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ctg gca acc act gtc 48  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
 1 5 10  
 gtt tcc ccc act aga gat cgt gca tct ggt gtc agg aat gtt gtt gca 96  
 Val Ser Pro Thr Arg Asp Arg Ala Ser Gly Val Arg Asn Val Val Ala  
 15 20 25 30  
 aca agc ttt cag act ctg acc cac gat gaa tgc tgt gca cac cct tcc 144  
 Thr Ser Phe Gln Thr Leu Thr His Asp Glu Cys Cys Ala His Pro Ser  
 35 40 45

tgt tgg aag gcc gaa gac ctg att tgt act aat caa cgt cgc agg acc 192  
 Cys Trp Lys Ala Glu Asp Leu Ile Cys Thr Asn Gln Arg Arg Arg Thr  
           50                          55                          60

ctc tgaaccacga cctcgag 212  
 Leu

<210> 449  
 <211> 63  
 <212> PRT  
 <213> Conus wittigi

<400> 449  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
   1                  5                          10                          15

Pro Thr Arg Asp Arg Ala Ser Gly Val Arg Asn Val Val Ala Thr Ser  
           20                          25                          30

Phe Gln Thr Leu Thr His Asp Glu Cys Cys Ala His Pro Ser Cys Trp  
           35                          40                          45

Lys Ala Glu Asp Leu Ile Cys Thr Asn Gln Arg Arg Arg Thr Leu  
           50                          55                          60

<210> 450  
 <211> 25  
 <212> PRT  
 <213> Conus wittigi

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> Xaa at residues 2 and 13 is Glu or gamma-carboxy-Glu; Xaa at  
           residue 7 is Pro or hydroxy-Pro; Xaa at residue 10 is Trp (D or L)  
           or bromo-Trp (D or L)

<400> 450  
 Asp Xaa Cys Cys Ala His Xaa Ser Cys Xaa Lys Ala Xaa Asp Leu Ile  
   1                  5                          10                          15

Cys Thr Asn Gln Arg Arg Arg Thr Leu  
           20                          25

<210> 451  
 <211> 230  
 <212> DNA  
 <213> Conus characteristicus

<220>  
 <221> CDS  
 <222> (7)..(195)

<400> 451  
 ggatcc atg ttc acc gtg ttt ctg ttg gtt gtc ttg gca acc act gtc 48  
           Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val  
           1                  5                          10

gtt tcc ttc act tca gat cgt gcg tct gaa ggc agg aat gct gca gcc 96  
 Val Ser Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Ala

15	20	25	30	
aag gac aaa gcg tct gac ctg gtg gct ctg aga gtc agg gga tgc tgt				144
Lys Asp Lys Ala Ser Asp Leu Val Ala Leu Arg Val Arg Gly Cys Cys				
	35	40	45	
gcc att cgt gaa tgt cgc ttg cag aat gca gcg tat tgt ggt gga ata				192
Ala Ile Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile				
	50	55	60	
tcc tgatgctcca ggaccctctg aaccacgacc tcgag				230
Ser				

<210> 452  
 <211> 63  
 <212> PRT  
 <213> Conus characteristicus

<400> 452  
 Met Phe Thr Val Phe Leu Leu Val Val Leu Ala Thr Thr Val Val Ser  
 1 5 10 15  
 Phe Thr Ser Asp Arg Ala Ser Glu Gly Arg Asn Ala Ala Ala Lys Asp  
 20 25 30  
 Lys Ala Ser Asp Leu Val Ala Leu Arg Val Arg Gly Cys Cys Ala Ile  
 35 40 45  
 Arg Glu Cys Arg Leu Gln Asn Ala Ala Tyr Cys Gly Gly Ile Ser  
 50 55 60

<210> 453  
 <211> 20  
 <212> PRT  
 <213> Conus characteristicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(20)  
 <223> Xaa at residue 7 is Glu or gamma-carboxy-Glu; Xaa at residue 15  
 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr  
 or O-phospho-Tyr

<400> 453  
 Gly Cys Cys Ala Ile Arg Xaa Cys Arg Leu Gln Asn Ala Ala Xaa Cys  
 1 5 10 15  
 Gly Gly Ile Ser  
 20

<210> 454  
 <211> 568  
 <212> DNA  
 <213> Conus betulinus

<220>  
 <221> CDS  
 <222> (395)..(508)  
 <220>

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<221> misc_feature
<222> (1)..(568)
<223> n is unknown
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[illegible]

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<210> 455
<211> 38
<212> PRT
<213> Conus betulinus
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<400>      455
Ser Gly Gly Arg Lys Ala Ala Ala Lys Ala Ser Asn Arg Ile Ala Leu
1              5              10              15

Thr Val Arg Ser Ala Thr Cys Cys Tyr Tyr Pro Pro Cys Tyr Glu Ala
                20              25              30

Tyr Pro Glu Ser Cys Leu
          35

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<210> 456
<211> 19
<212> PRT
<213> Conus betulinus
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<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residues 12 and 16 is Glu or gamma-carboxy-Glu; Xaa at
      residues 8, 9 and 13 is Pro or hydroxy-Pro; Xaa at residues 6, 7,
      11 and 14 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
      O-sulpho-Tyr or O-phospho-Tyr

```

<400> 456



Ser Ala Thr Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Xaa Xaa  
 1 5 10 15

Ser Cys Leu

<210> 457

<211> 29

<212> PRT

<213> Conus textile

<400> 457

Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys  
 1 5 10 15

Asp Trp Trp Thr Cys Ser Ala Arg Thr Asn Arg Cys Phe  
 20 25

<210> 458

<211> 31

<212> PRT

<213> Conus ammiralis

<400> 458

Gly Met Trp Gly Asp Cys Lys Asp Gly Leu Thr Thr Cys Phe Ala Pro  
 1 5 10 15

Ser Glu Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp  
 20 25 30

<210> 459

<211> 36

<212> PRT

<213> Conus ammiralis

<400> 459

Trp Arg Glu Gly Ser Cys Thr Ser Trp Leu Ala Thr Cys Thr Gln Asp  
 1 5 10 15

Gln Gln Cys Cys Thr Asp Val Cys Tyr Lys Arg Asp Tyr Cys Ala Leu  
 20 25 30

Trp Asp Asp Arg  
 35

<210> 460

<211> 25

<212> PRT

<213> Conus ammiralis

<400> 460

Asn Cys Ser Asp Asp Trp Gln Tyr Cys Glu Ser Pro Ser Asp Cys Cys  
 1 5 10 15

Ser Trp Asp Cys Asp Val Val Cys Ser  
 20 25

<210> 461

<211> 39

<212> PRT

<213> Conus ammiralis

&lt;400&gt; 461

Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Lys Cys Ser Lys  
 1 5 10 15

Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Ile Thr Arg Cys Glu Leu  
 20 25 30

Met Arg Phe Pro Pro Asp Trp  
 35

&lt;210&gt; 462

&lt;211&gt; 29

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 462

Asp Cys Arg Gly Tyr Asp Ala Pro Cys Ser Ser Gly Ala Pro Cys Cys  
 1 5 10 15

Asp Trp Trp Thr Cys Ser Ala Arg Thr Gly Arg Cys Phe  
 20 25

&lt;210&gt; 463

&lt;211&gt; 26

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 463

Leu Cys Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys  
 1 5 10 15

Ser Trp Asn Cys His Asn Gly His Cys Thr  
 20 25

&lt;210&gt; 464

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus ammiralis

&lt;400&gt; 464

Cys Ser Ser Trp Ala Lys Tyr Cys Glu Val Asp Ser Glu Cys Cys Ser  
 1 5 10 15

Glu Gln Cys Val Arg Ser Tyr Cys Ala Met Trp  
 20 25

&lt;210&gt; 465

&lt;211&gt; 32

&lt;212&gt; PRT

&lt;213&gt; Conus pennaceus

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(32)

&lt;223&gt; Xaa at residues 14 and 26 is gamma-carboxy-Glu; Xaa at residue 31 is hydroxy-Pro

&lt;400&gt; 465

Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys

1 5 10 15

Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
20 25 30

<210> 466  
 <211> 32  
 <212> PRT  
 <213> Conus gloriamaris

<400> 466  
 Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser Pro Gly Ala Gln Cys Cys  
1 5 10 15

Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu  
20 25 30

<210> 467  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa is gamma-carboxy-Glu

<400> 467  
 Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr  
1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 468  
 <211> 29  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa is gamma-carboxy-Glu

<400> 468  
 Asn Gly Gln Cys Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Xaa  
1 5 10 15

Cys Cys Ser Leu Asp Cys Glu Met Tyr Cys Thr Gln Ile  
20 25

<210> 469  
 <211> 27  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa is gamma-carboxy-Glu

&lt;400&gt; 469

Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Xaa Cys Cys Ser  
 1 5 10 15

Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe  
 20 25

&lt;210&gt; 470

&lt;211&gt; 26

&lt;212&gt; PRT

<213> *Conus marmoreus*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(26)

&lt;223&gt; Xaa is gamma-carboxy-Glu

&lt;400&gt; 470

Asn Gly Gly Cys Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Xaa  
 1 5 10 15

Cys Cys Ser Met Ser Cys Asp Met Tyr Cys  
 20 25

&lt;210&gt; 471

&lt;211&gt; 33

&lt;212&gt; PRT

<213> *Conus radiatus*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(33)

&lt;223&gt; Xaa at residues 1, 10 and 33 is bromo-Trp; Xaa at residues 5, 6, 15 and 26 is gamma-carboxy-Glu

&lt;400&gt; 471

Xaa Phe Gly His Xaa Xaa Cys Thr Tyr Xaa Leu Gly Pro Cys Xaa Val  
 1 5 10 15

Asp Asp Thr Cys Cys Ser Ala Ser Cys Xaa Ser Lys Phe Cys Gly Leu  
 20 25 30

Xaa

&lt;210&gt; 472

&lt;211&gt; 31

&lt;212&gt; PRT

<213> *Conus radiatus*

&lt;400&gt; 472

Trp Trp Gly Glu Cys Ser Asn Trp Leu Gly Ser Cys Ser Thr Pro  
 1 5 10 15

Ser Asn Cys Cys Leu Lys Ser Cys Asn Gly His Cys Thr Leu Trp  
 20 25 30

&lt;210&gt; 473

&lt;211&gt; 26

&lt;212&gt; PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(26)

<223> Xaa at residues 3 and 8 is hydroxy-Pro; Xaa at residues 7 and 14  
is gamma-carboxy-Glu

<400> 473

Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys  
1 5 10 15

Ser Trp Asn Cys Tyr Asn Gly His Cys Thr  
20 25

<210> 474

<211> 28

<212> PRT

<213> Conus textile

<400> 474

Asp Cys Tyr Ser Trp Leu Gly Ser Cys Ile Ala Pro Ser Gln Cys Cys  
1 5 10 15

Ser Glu Val Cys Asp Tyr Tyr Cys Arg Leu Trp Arg  
20 25

<210> 475

<211> 34

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(34)

<223> Xaa is gamma-carboxy-Glu

<400> 475

Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser Xaa  
1 5 10 15

Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro Pro  
20 25 30

Asp Trp

<210> 476

<211> 31

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(31)

<223> Xaa is gamma-carboxy-Glu

<400> 476

Gly Met Trp Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro  
1 5 10 15

Ser Xaa Cys Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp  
                   20                  25                  30

<210> 477  
 <211> 34  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa is gamma-carboxy-Glu

<400> 477  
 Asp Trp Trp Asp Asp Gly Cys Ser Val Trp Gly Pro Cys Thr Val Asn  
 1                  5                  10                  15

Ala Xaa Cys Cys Ser Gly Asp Cys His Glu Thr Cys Ile Phe Gly Trp  
                   20                  25                  30

Glu Val

<210> 478  
 <211> 39  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(39)  
 <223> Xaa is gamma-carboxy-Glu

<400> 478  
 Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu Cys Ser Arg  
 1                  5                  10                  15

Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Glu Leu  
                   20                  25                  30

Met Pro Phe Pro Pro Asp Trp  
                   35

<210> 479  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa is gamma-carboxy-Glu

<400> 479  
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser  
 1                  5                  10                  15

Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe  
                   20                  25

<210> 480

<211> 43  
 <212> PRT  
 <213> Conus characteristicus

<400> 480  
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Tyr Arg Gly Cys Thr Cys Ser Cys Gln  
 35 40

<210> 481  
 <211> 42  
 <212> PRT  
 <213> Conus characteristicus

<400> 481  
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys  
 35 40

<210> 482  
 <211> 42  
 <212> PRT  
 <213> Conus characteristicus

<400> 482  
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys  
 35 40

<210> 483  
 <211> 42  
 <212> PRT  
 <213> Conus characteristicus

<400> 483  
 Gly Cys Ser Gly Thr Cys Arg Arg His Arg Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys  
 35 40

<210> 484

<211> 42  
 <212> PRT  
 <213> *Conus characteristicus*

<400> 484  
 Gly Cys Ser Gly Thr Cys His Arg Arg Glu Asp Gly Lys Cys Arg Gly  
 1 5 10 15  
 Thr Cys Asp Cys Ser Gly Tyr Ser Tyr Cys Arg Cys Gly Asp Ala His  
 20 25 30  
 His Phe Tyr Arg Gly Cys Thr Cys Thr Cys  
 35 40

<210> 485  
 <211> 42  
 <212> PRT  
 <213> *Conus characteristicus*

<400> 485  
 Gly Cys Ser Gly Thr Cys His Arg Arg Gln Asn Gly Glu Cys Gln Gly  
 1 5 10 15  
 Thr Cys Asp Cys Asp Gly His Asp His Cys Asp Cys Gly Asp Thr Leu  
 20 25 30  
 Gly Thr Tyr Ser Gly Cys Val Cys Ile Cys  
 35 40

<210> 486  
 <211> 45  
 <212> PRT  
 <213> *Conus lacterculatus*

<400> 486  
 Gln Ser Glu Thr Ala Cys Arg Ser Leu Gly Ser Tyr Gln Cys Met Gly  
 1 5 10 15  
 Lys Cys Gln Leu Gly Val His Ser Trp Cys Glu Cys Ile Tyr Asn Arg  
 20 25 30  
 Gly Ser Gln Lys Ser Gly Cys Ala Cys Arg Cys Gln Lys  
 35 40 45

<210> 487  
 <211> 48  
 <212> PRT  
 <213> *Conus monachus*

<400> 487  
 Gln Cys Thr Leu Val Asn Asn Cys Asp Arg Asn Gly Glu Arg Ala Cys  
 1 5 10 15  
 Asn Gly Asp Cys Ser Cys Glu Gly Gln Ile Cys Lys Cys Gly Tyr Arg  
 20 25 30  
 Val Ser Pro Gly Lys Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
 35 40 45

<210> 488



<211> 41  
 <212> PRT  
 <213> *Conus purpurascens*

<400> 488  
 Gly Cys Ser Gly Ser Pro Cys Phe Lys Asn Lys Thr Cys Arg Asp Glu  
 1 5 10 15  
 Cys Ile Cys Gly Gly Leu Ser Asn Cys Trp Cys Gly Tyr Gly Gly Ser  
 20 25 30  
 Arg Gly Cys Lys Cys Thr Cys Arg Glu  
 35 40

<210> 489  
 <211> 47  
 <212> PRT  
 <213> *Conus radiatus*

<400> 489  
 Lys Cys Asn Phe Asp Lys Cys Lys Gly Thr Gly Val Tyr Asn Cys Gly  
 1 5 10 15  
 Glu Ser Cys Ser Cys Glu Gly Leu His Ser Cys Arg Cys Thr Tyr Asn  
 20 25 30  
 Ile Gly Ser Met Lys Ser Gly Cys Ala Cys Ile Cys Thr Tyr Tyr  
 35 40 45

<210> 490  
 <211> 44  
 <212> PRT  
 <213> *Conus radiatus*

<400> 490  
 Tyr Gly Leu Gly Cys Ala Gly Thr Cys Gly Ser Ser Ser Asn Cys Val  
 1 5 10 15  
 Arg Asp Tyr Cys Asp Cys Pro Lys Pro Asn Cys Tyr Cys Thr Gly Lys  
 20 25 30  
 Gly Phe Arg Gln Pro Gly Cys Gly Cys Ser Cys Leu  
 35 40

<210> 491  
 <211> 46  
 <212> PRT  
 <213> *Conus striolatus*

<400> 491  
 Gln Cys Thr Phe Val Asn Asn Cys Gln Gln Asn Gly Cys Ala Asn Gly  
 1 5 10 15  
 Asp Cys Ser Cys Gly Asp Gln Ile Cys Lys Cys Gly Tyr Arg Ile Ser  
 20 25 30  
 Pro Gly Arg Ser Gly Cys Ala Cys Thr Cys Arg Asn Ala Lys  
 35 40 45

<210> 492  
 <211> 44

<212> PRT

<213> Conus tulipa

<400> 492

Phe Gly Pro Ile Cys Thr Cys Phe Lys Ser Gln Asn Cys Arg Gly Ser  
1 5 10 15

Cys Glu Cys Met Ser Pro Pro Gly Cys Tyr Cys Ser Asn Asn Gly Ile  
20 25 30

Arg Glu Arg Gly Cys Ser Cys Thr Cys Pro Gly Thr  
35 40

<210> 493

<211> 46

<212> PRT

<213> Conus tulipa

<400> 493

Gly Cys Thr Gly Asn Cys Asp Trp Thr Cys Ser Gly Asp Cys Ser Cys  
1 5 10 15

Gln Gly Thr Ser Asp Ser Cys His Cys Ile Pro Pro Lys Ser Ile Gly  
20 25 30

Asn Arg Cys Arg Cys Gln Cys Lys Arg Lys Ile Glu Ile Asp  
35 40 45

<210> 494

<211> 15

<212> PRT

<213> Conus textile

<400> 494

Glu Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu Thr  
1 5 10 15

<210> 495

<211> 15

<212> PRT

<213> Conus textile

<400> 495

Gly Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu Thr  
1 5 10 15

<210> 496

<211> 20

<212> PRT

<213> Conus marmoreus

<400> 496

Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Glu Ile Lys  
1 5 10 15

Glu Asn Asp Phe  
20

<210> 497

<211> 11

<212> PRT  
 <213> *Conus marmoreus*

<400> 497  
 Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser  
 1 5 10

<210> 498  
 <211> 10  
 <212> PRT  
 <213> *Conus marmoreus*

<400> 498  
 Asn Ala Cys Cys Ile Val Arg Gln Cys Cys  
 1 5 10

<210> 499  
 <211> 10  
 <212> PRT  
 <213> *Conus quercinus*

<400> 499  
 Gly Cys Cys Ala Arg Leu Thr Cys Cys Val  
 1 5 10

<210> 500  
 <211> 10  
 <212> PRT  
 <213> *Conus quercinus*

<400> 500  
 Gly Cys Cys Ala Met Leu Thr Cys Cys Val  
 1 5 10

<210> 501  
 <211> 12  
 <212> PRT  
 <213> *Conus purpurascens*

<400> 501  
 Gly Cys Cys Pro Lys Gln Met Arg Cys Cys Thr Leu  
 1 5 10

<210> 502  
 <211> 11  
 <212> PRT  
 <213> *Conus characteristicus*

<400> 502  
 Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile  
 1 5 10

<210> 503  
 <211> 10  
 <212> PRT  
 <213> *Conus characteristicus*

<400> 503  
 Cys Cys Pro Asn Lys Pro Cys Cys Phe Ile  
 1 5 10

<210> 504  
 <211> 13  
 <212> PRT  
 <213> Conus geographus

<400> 504  
 Glx Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile  
 1 5 10

<210> 505  
 <211> 13  
 <212> PRT  
 <213> Conus geographus

<400> 505  
 Glx Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val  
 1 5 10

<210> 506  
 <211> 15  
 <212> PRT  
 <213> Conus imperialis

<400> 506  
 Asp Trp Asn Ser Cys Cys Gly Lys Asn Pro Gly Cys Cys Pro Trp  
 1 5 10 15

<210> 507  
 <211> 11  
 <212> PRT  
 <213> Conus betulinus

<400> 507  
 Asn Cys Cys Pro Asp Ser Pro Pro Cys Cys His  
 1 5 10

<210> 508  
 <211> 12  
 <212> PRT  
 <213> Conus ammiralis

<400> 508  
 Gly Asn Cys Cys Glu Phe Trp Glu Phe Cys Cys Asp  
 1 5 10

<210> 509  
 <211> 9  
 <212> PRT  
 <213> Conus dalli

<400> 509  
 Cys Cys Glu Tyr Trp Lys Leu Cys Cys  
 1 5

<210> 510  
 <211> 11  
 <212> PRT  
 <213> Conus omaria

<400> 510  
 Val Cys Cys Gly Tyr Lys Phe Phe Cys Cys Arg  
 1 5 10

<210> 511  
 <211> 11  
 <212> PRT  
 <213> *Conus aulicus*

<400> 511  
 Phe Cys Cys Pro Val Ile Arg Tyr Cys Cys Trp  
 1 5 10

<210> 512  
 <211> 11  
 <212> PRT  
 <213> *Conus aulicus*

<400> 512  
 Phe Cys Cys Pro Phe Ile Arg Tyr Cys Cys Trp  
 1 5 10

<210> 513  
 <211> 10  
 <212> PRT  
 <213> *Conus aulicus*

<400> 513  
 Cys Cys Pro Met Ile Tyr Trp Cys Cys Ser  
 1 5 10

<210> 514  
 <211> 10  
 <212> PRT  
 <213> *Conus aulicus*

<400> 514  
 Cys Cys Pro Glu Ile Tyr Trp Cys Cys Ser  
 1 5 10

<210> 515  
 <211> 10  
 <212> PRT  
 <213> *Conus nobilis*

<400> 515  
 Ile Cys Cys Pro Ile Ile Leu Trp Cys Cys  
 1 5 10

<210> 516  
 <211> 9  
 <212> PRT  
 <213> *Conus ammiralis*

<400> 516  
 Cys Cys Pro Pro Val Ile Trp Cys Cys  
 1 5

<210> 517  
 <211> 11

<212> PRT  
 <213> Conus textile

<400> 517  
 Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln  
 1 5 10

<210> 518  
 <211> 13  
 <212> PRT  
 <213> Conus aulicus

<400> 518  
 Trp Asn Asn Tyr Cys Cys Thr Asn Glu Leu Trp Cys Cys  
 1 5 10

<210> 519  
 <211> 13  
 <212> PRT  
 <213> Conus gloriamaris

<400> 519  
 Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp Trp  
 1 5 10

<210> 520  
 <211> 11  
 <212> PRT  
 <213> Conus gloriamaris

<400> 520  
 Val Cys Cys Arg Pro Val Gln Asp Cys Cys Ser  
 1 5 10

<210> 521  
 <211> 13  
 <212> PRT  
 <213> Conus dalli

<400> 521  
 Pro Val Asn Cys Cys Pro Ile Asp Gln Ser Cys Cys Ser  
 1 5 10

<210> 522  
 <211> 17  
 <212> PRT  
 <213> Conus spurius

<400> 522  
 Gly Asn Ile His Cys Cys Thr Lys Tyr Gln Pro Cys Cys Ser Ser Pro  
 1 5 10 15

Ser

<210> 523  
 <211> 12  
 <212> PRT  
 <213> Conus textile

<400> 523

Glx Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys  
 1 5 10

<210> 524  
 <211> 11  
 <212> PRT  
 <213> Conus bandanus

<400> 524  
 Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys  
 1 5 10

<210> 525  
 <211> 13  
 <212> PRT  
 <213> Conus pennaceus

<400> 525  
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg  
 1 5 10

<210> 526  
 <211> 13  
 <212> PRT  
 <213> Conus pennaceus

<400> 526  
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Ser  
 1 5 10

<210> 527  
 <211> 12  
 <212> PRT  
 <213> Conus pennaceus

<400> 527  
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys  
 1 5 10

<210> 528  
 <211> 12  
 <212> PRT  
 <213> Conus episcopatus

<400> 528  
 Ser Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys  
 1 5 10

<210> 529  
 <211> 13  
 <212> PRT  
 <213> Conus marmoreus

<400> 529  
 Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys Leu Pro Cys  
 1 5 10

<210> 530  
 <211> 12  
 <212> PRT

<213> Conus pennaceus

<400> 530

Leu Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn  
1 5 10

<210> 531

<211> 13

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa is hydroxy-Pro

<400> 531

Asn Gly Val Cys Cys Gly Tyr Lys Leu Cys His Xaa Cys  
1 5 10

<210> 532

<211> 12

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> Xaa is hydroxy-Pro

<400> 532

Gly Val Cys Cys Gly Tyr Lys Leu Cys His Xaa Cys  
1 5 10

<210> 533

<211> 11

<212> PRT

<213> Conus bandanus

<400> 533

Ala Cys Cys Gly Tyr Lys Leu Cys Ser Pro Cys  
1 5 10

<210> 534

<211> 12

<212> PRT

<213> Conus aulicus

<400> 534

Ser Val Cys Cys Gly Tyr Lys Leu Cys Phe Pro Cys  
1 5 10

<210> 535

<211> 13

<212> PRT

<213> Conus textile

<400> 535

Asn Gly Val Cys Cys Gly Tyr Arg Met Cys Val Pro Cys  
1 5 10



<210> 536  
 <211> 12  
 <212> PRT  
 <213> *Conus textile*

<400> 536  
 Glx Thr Cys Cys Gly Tyr Arg Met Cys Val Pro Cys  
 1 5 10

<210> 537  
 <211> 12  
 <212> PRT  
 <213> *Conus ammiralis*

<400> 537  
 Glx Ala Cys Cys Gly Phe Lys Met Cys Val Pro Cys  
 1 5 10

<210> 538  
 <211> 13  
 <212> PRT  
 <213> *Conus pennaceus*

<400> 538  
 Ser Thr Cys Cys Gly Phe Lys Met Cys Ile Pro Cys Arg  
 1 5 10

<210> 539  
 <211> 14  
 <212> PRT  
 <213> *Conus pennaceus*

<400> 539  
 Asn Gly Val Cys Cys Gly Phe Trp Met Cys Ile Pro Cys Asn  
 1 5 10

<210> 540  
 <211> 12  
 <212> PRT  
 <213> *Conus omaria*

<400> 540  
 Asp Val Cys Cys Tyr Val Arg Met Cys Pro Cys Arg  
 1 5 10

<210> 541  
 <211> 7  
 <212> PRT  
 <213> *Conus imperialis*

<400> 541  
 Glx Cys Gly Gln Ala Trp Cys  
 1 5

<210> 542  
 <211> 8  
 <212> PRT  
 <213> *Conus stercusmuscarum*

<220>  
 <221> PEPTIDE  
 <222> (1)..(8)  
 <223> Xaa is hydroxy-Pro

<400> 542

Gly Cys Xaa Trp Gln Pro Val Cys  
 1 5

<210> 543  
 <211> 11  
 <212> PRT  
 <213> Conus arenatus

<220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> Xaa is hydroxy-Pro

<400> 543  
 Glx Tyr Gly Cys Xaa Xaa Gly Leu Trp Cys His  
 1 5 10

<210> 544  
 <211> 10  
 <212> PRT  
 <213> Conus arenatus

<400> 544  
 Ala Ser Gly Cys Pro Trp Arg Pro Trp Cys  
 1 5 10

<210> 545  
 <211> 11  
 <212> PRT  
 <213> Conus arenatus

<400> 545  
 Glx Tyr Gly Cys Pro Val Gly Leu Trp Cys Asp  
 1 5 10

<210> 546  
 <211> 9  
 <212> PRT  
 <213> Conus arenatus

<400> 546  
 Ser Gly Cys Pro Trp Gln Pro Trp Cys  
 1 5

<210> 547  
 <211> 9  
 <212> PRT  
 <213> Conus arenatus

<400> 547  
 Ser Gly Cys Pro Trp His Pro Trp Cys  
 1 5

<210> 548  
 <211> 30  
 <212> PRT  
 <213> *Conus ermineus*

<220>  
 <221> PEPTIDE  
 <222> (1)..(30)  
 <223> Xaa is hydroxy-Pro

<400> 548  
 Gly Cys Cys Gly Lys Tyr Xaa Asn Ala Ala Cys His Xaa Cys Gly Cys  
 1 5 10 15  
 Thr Val Gly Arg Xaa Xaa Tyr Cys Asp Arg Xaa Ser Gly Gly  
 20 25 30

<210> 549  
 <211> 25  
 <212> PRT  
 <213> *Conus purpurascens*

<400> 549  
 Gly Cys Cys Gly Ser Tyr Pro Asn Ala Ala Cys His Pro Cys Gly Cys  
 1 5 10 15  
 Lys Asp Arg Pro Ser Tyr Cys Gly Gln  
 20 25

<210> 550  
 <211> 23  
 <212> PRT  
 <213> *Conus purpurascens*

<400> 550  
 Glu Gly Cys Cys Ser Asn Pro Ala Cys His Pro Cys Gly Cys Lys Asp  
 1 5 10 15  
 Arg Pro Ser Tyr Cys Gly Gln  
 20

<210> 551  
 <211> 32  
 <212> PRT  
 <213> *Conus arenatus*

<400> 551  
 Val Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Glu Glu Glu Lys His  
 1 5 10 15  
 Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp  
 20 25 30

<210> 552  
 <211> 32  
 <212> PRT  
 <213> *Conus arenatus*

<400> 552  
 Ile Val Thr Glu Ala Cys Glu Glu Ser Cys Glu Asp Glu Glu Lys His

1 5 10 15

Cys Cys His Val Asn Asn Gly Val Pro Ser Cys Ala Val Ile Cys Trp  
20 25 30

<210> 553  
<211> 32  
<212> PRT  
<213> Conus arenatus

<400> 553  
Ile Val Thr Glu Ala Cys Glu Glu His Cys Glu Asp Glu Glu Gln Phe  
1 5 10 15

Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Pro Val Cys Phe  
20 25 30

<210> 554  
<211> 32  
<212> PRT  
<213> Conus arenatus

<400> 554  
Val Val Thr Gly Ala Cys Glu Glu His Cys Glu Asp Glu Glu Lys His  
1 5 10 15

Cys Cys Gly Leu Glu Asn Gly Gln Pro Phe Cys Ala Arg Leu Cys Leu  
20 25 30

<210> 555  
<211> 32  
<212> PRT  
<213> Conus distans

<400> 555  
Asn Val Asp Gln Glu Cys Ile Asp Ala Cys Gln Leu Glu Asp Lys Asn  
1 5 10 15

Cys Cys Gly Arg Thr Asp Gly Glu Pro Arg Cys Ala Lys Ile Cys Leu  
20 25 30

<210> 556  
<211> 32  
<212> PRT  
<213> Conus distans

<400> 556  
Glu Thr Asp Gln Glu Cys Ile Asp Ile Cys Lys Gln Glu Asp Lys Lys  
1 5 10 15

Cys Cys Gly Arg Ser Asn Gly Glu Pro Thr Cys Ala Lys Ile Cys Leu  
20 25 30

<210> 557  
<211> 32  
<212> PRT  
<213> Conus distans

<400> 557  
Glu Thr Asp Gln Glu Cys Ile Asp Thr Cys Glu Gln Glu Asp Lys Lys

1	5	10	15
Cys Cys Gly Arg Thr Asn Gly Glu Pro Val Cys Ala Lys Ile Cys Phe			
20		25	30

<210> 558  
 <211> 37  
 <212> PRT  
 <213> Conus purpurascens

<400> 558
Pro Lys Thr Glu Ala Cys Glu Glu Val Cys Glu Leu Glu Glu Lys His
1 5 10 15

Cys Cys Cys Ile Arg Ser Asp Gly Pro Lys Cys Ser Arg Lys Cys Leu
20 25 30

Leu Ser Ile Phe Cys
35

<210> 559  
 <211> 32  
 <212> PRT  
 <213> Conus purpurascens

<400> 559
Val Val Ser Glu Glu Cys Lys Lys Tyr Cys Lys Lys Gln Asn Lys Asn
1 5 10 15

Cys Cys Ser Ser Lys His Glu Glu Pro Arg Cys Ala Lys Ile Cys Phe
20 25 30

<210> 560  
 <211> 32  
 <212> PRT  
 <213> Conus sponsalis

<400> 560
Ala Val Thr Glu Ala Cys Thr Glu Asp Cys Lys Thr Gln Asp Lys Lys
1 5 10 15

Cys Cys Gly Glu Met Asn Gly Gln His Thr Cys Ala Lys Ile Cys Leu
20 25 30

<210> 561  
 <211> 37  
 <212> PRT  
 <213> Conus tulipa

<400> 561
Pro Lys Thr Lys Glu Cys Glu Arg Tyr Cys Glu Leu Glu Glu Lys His
1 5 10 15

Cys Cys Cys Ile Arg Ser Asn Gly Pro Lys Cys Ser Arg Ile Cys Ile
20 25 30

Phe Lys Phe Trp Cys
35

<210> 562

<211> 36  
 <212> PRT  
 <213> *Conus tulipa*

<400> 562  
 Pro Lys Thr Arg Glu Cys Glu Met Gln Cys Glu Gln Glu Glu Lys His  
 1 5 10 15  
 Cys Cys Arg Val Arg Asp Gly Thr Gly Gln Cys Ala Pro Lys Cys Leu  
 20 25 30

Gly Ile Asn Trp  
 35

<210> 563  
 <211> 9  
 <212> PRT  
 <213> *Conus geographus*

<400> 563  
 Cys Phe Ile Arg Asn Cys Pro Lys Gly  
 1 5

<210> 564  
 <211> 9  
 <212> PRT  
 <213> *Conus striatus*

<400> 564  
 Cys Ile Ile Arg Asn Cys Pro Arg Gly  
 1 5

<210> 565  
 <211> 28  
 <212> PRT  
 <213> *Conus arenatus*

<400> 565  
 Gly Cys Thr Pro Pro Gly Gly Val Cys Gly Tyr His Gly His Cys Cys  
 1 5 10 15

Asp Phe Cys Asp Thr Phe Gly Asn Leu Cys Val Ser  
 20 25

<210> 566  
 <211> 27  
 <212> PRT  
 <213> *Conus geographus*

<400> 566  
 Ala Cys Ser Gly Arg Gly Ser Arg Cys Pro Pro Gln Cys Cys Met Gly  
 1 5 10 15

Leu Thr Cys Gly Arg Glu Tyr Pro Pro Arg Cys  
 20 25

<210> 567  
 <211> 31  
 <212> PRT  
 <213> *Conus characteristicus*

&lt;400&gt; 567

Asn Cys Gly Glu Gln Gly Glu Gly Cys Ala Thr Arg Pro Cys Cys Ser  
 1 5 10 15

Gly Leu Ser Cys Val Gly Ser Arg Pro Gly Gly Leu Cys Gln Tyr  
 20 25 30

&lt;210&gt; 568

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Conus textile

&lt;400&gt; 568

Asn Cys Pro Tyr Cys Val Val Tyr Cys Cys Pro Pro Ala Tyr Cys Glu  
 1 5 10 15

Ala Ser Gly Cys Arg Pro Pro  
 20

&lt;210&gt; 569

&lt;211&gt; 27

&lt;212&gt; PRT

&lt;213&gt; Conus delesstii

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(27)

&lt;223&gt; Xaa at residue 4 is hydroxy-Pro; Xaa at residues 13 and 16 is gamm-carboxy-Glu

&lt;400&gt; 569

Ala Cys Lys Xaa Lys Asn Asn Leu Cys Ala Ile Thr Xaa Met Ala Xaa  
 1 5 10 15

Cys Cys Ser Gly Phe Cys Leu Ile Tyr Arg Cys  
 20 25

&lt;210&gt; 570

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Conus lividus

&lt;400&gt; 570

Ser Cys Gly His Ser Gly Ala Gly Cys Tyr Thr Arg Pro Cys Cys Pro  
 1 5 10 15

Gly Leu His Cys Ser Gly Gly Gln Ala Gly Gly Leu Cys Val  
 20 25 30

&lt;210&gt; 571

&lt;211&gt; 35

&lt;212&gt; PRT

&lt;213&gt; Conus lividus

&lt;400&gt; 571

Asp Cys Gly Glu Ser Gly Gln Gly Cys Tyr Ser Val Arg Pro Cys Cys  
 1 5 10 15

Pro Gly Leu Ile Cys Lys Gly Thr Gly Gly Gly Gly Leu Cys Arg Pro  
 20 25 30

Ser Gly Ile  
35

<210> 572  
<211> 31  
<212> PRT  
<213> *Conus miliaris*

<400> 572  
Cys Thr Pro Pro Gly Gly Leu Cys Tyr His Ala Tyr Pro Cys Cys Ser  
1 5 10 15

Lys Thr Cys Asn Leu Asp Thr Ser Gln Cys Glu Pro Arg Trp Ser  
20 25 30

<210> 573  
<211> 36  
<212> PRT  
<213> *Conus miles*

<400> 573  
Cys Thr Asp Asp Ser Gln Phe Cys Asn Pro Ser Asn His Asp Cys Cys  
1 5 10 15

Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile Cys Ala Ile Val  
20 25 30

Pro Glu Asn Ser  
35

<210> 574  
<211> 36  
<212> PRT  
<213> *Conus miles*

<400> 574  
Cys Thr Glu Asp Ser Gln Phe Cys Asn Pro Ser Asn His Asp Cys Cys  
1 5 10 15

Ser Gly Lys Cys Ile Asp Glu Gly Asp Asn Gly Ile Cys Ala Ile Val  
20 25 30

Pro Glu Asn Ser  
35

<210> 575  
<211> 30  
<212> PRT  
<213> *Conus pulicarius*

<400> 575  
Cys Ser Asp Phe Gly Ser Asp Cys Val Pro Ala Thr His Asn Cys Cys  
1 5 10 15

Ser Gly Glu Cys Phe Gly Phe Glu Asp Phe Gly Leu Cys Thr  
20 25 30

<210> 576  
<211> 30



<212> PRT  
 <213> Conus quercinus

<400> 576  
 Ala Cys Ser Gln Val Gly Glu Ala Cys Phe Pro Gln Lys Pro Cys Cys  
 1 5 10 15  
 Pro Gly Phe Leu Cys Asn His Ile Gly Gly Met Cys His His  
 20 25 30

<210> 577  
 <211> 28  
 <212> PRT  
 <213> Conus striatus

<400> 577  
 Cys Leu Pro Asp Gly Thr Ser Cys Leu Phe Ser Arg Ile Arg Cys Cys  
 1 5 10 15  
 Gly Thr Cys Ser Ser Ile Leu Lys Ser Cys Val Ser  
 20 25

<210> 578  
 <211> 31  
 <212> PRT  
 <213> Conus tessulatus

<400> 578  
 Ser Cys Ala Glu Phe Gly Glu Val Cys Ser Ser Thr Ala Cys Cys Pro  
 1 5 10 15  
 Asp Leu Asp Cys Val Glu Ala Tyr Ser Pro Ile Cys Leu Trp Glu  
 20 25 30

<210> 579  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<400> 579  
 Lys Cys Val Glu Gln Trp Lys Tyr Cys Thr Arg Glu Ser Leu Cys Cys  
 1 5 10 15  
 Ala Gly Leu Cys Leu Phe Ser Phe Cys Ile Leu  
 20 25

<210> 580  
 <211> 29  
 <212> PRT  
 <213> Conus textile

<400> 580  
 Cys Val Glu Gln Trp Glu Val Cys Gly Ile Ile Leu Phe Ser Ser Ser  
 1 5 10 15  
 Cys Cys Gly Gln Leu Cys Leu Phe Gly Phe Cys Val Leu  
 20 25

<210> 581  
 <211> 32

<212> PRT  
 <213> *Conus virgo*

<400> 581  
 Asp Cys Gly Gly Gln Gly Glu Gly Cys Tyr Thr Gln Pro Cys Cys Pro  
 1 5 10 15  
 Gly Leu Arg Cys Arg Gly Gly Gly Thr Gly Gly Gly Val Cys Gln Leu  
 20 25 30

<210> 582  
 <211> 33  
 <212> PRT  
 <213> *Conus wittigi*

<400> 582  
 Phe Gly Ser Phe Ile Pro Cys Ala Arg Leu Gly Glu Pro Cys Thr Ile  
 1 5 10 15  
 Cys Cys Arg Pro Leu Arg Cys Arg Glu Ser Gly Thr Pro Thr Cys Gln  
 20 25 30

Val

<210> 583  
 <211> 30  
 <212> PRT  
 <213> *Conus regius*

<400> 583  
 Thr Cys Leu Glu His Asn Lys Leu Cys Trp Tyr Asp Arg Asp Cys Cys  
 1 5 10 15  
 Thr Ile Tyr Cys Asn Glu Asn Lys Cys Gly Val Lys Pro Gln  
 20 25 30

<210> 584  
 <211> 34  
 <212> PRT  
 <213> *Conus radiatus*

<400> 584  
 Ala Cys Lys Ser Asn Tyr Asp Cys Pro Gln Arg Phe Lys Cys Cys Ser  
 1 5 10 15  
 Tyr Thr Trp Asn Gly Ser Ser Gly Tyr Cys Lys Arg Val Cys Tyr Leu  
 20 25 30

Tyr Arg

<210> 585  
 <211> 24  
 <212> PRT  
 <213> *Conus purpurascens*

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa is hydroxy-Pro

&lt;400&gt; 585

Gly Xaa Xaa Cys Cys Leu Tyr Gly Ser Cys Arg Xaa Phe Xaa Gly Cys  
 1 5 10 15

Tyr Asn Ala Leu Cys Cys Arg Lys  
 20

&lt;210&gt; 586

&lt;211&gt; 24

&lt;212&gt; PRT

<213> *Conus purpurascens*

&lt;400&gt; 586

His Pro Pro Cys Cys Met Tyr Gly Arg Cys Arg Arg Tyr Pro Gly Cys  
 1 5 10 15

Ser Ser Ala Ser Cys Cys Gln Gly  
 20

&lt;210&gt; 587

&lt;211&gt; 36

&lt;212&gt; PRT

<213> *Conus consors*

&lt;400&gt; 587

Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp  
 1 5 10 15

Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro Pro  
 20 25 30

Lys Arg Lys Pro  
 35

&lt;210&gt; 588

&lt;211&gt; 39

&lt;212&gt; PRT

<213> *Conus aurisiacus*

&lt;400&gt; 588

Glx Ser Trp Leu Val Pro Ser Thr Ile Thr Thr Cys Cys Gly Tyr Asp  
 1 5 10 15

Pro Gly Thr Met Cys Pro Pro Cys Arg Cys Asn Asn Thr Cys Lys Pro  
 20 25 30

Lys Lys Pro Lys Pro Gly Lys  
 35

&lt;210&gt; 589

&lt;211&gt; 37

&lt;212&gt; PRT

<213> *Conus consors*

&lt;400&gt; 589

Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp  
 1 5 10 15

Pro Met Thr Trp Cys Pro Ser Cys Met Cys Thr Tyr Ser Cys Pro His  
 20 25 30

Gln Arg Lys Lys Pro  
35

<210> 590  
<211> 36  
<212> PRT  
<213> Conus magus

<400> 590  
Ala Pro Glu Leu Val Val Thr Ala Thr Thr Thr Cys Cys Gly Tyr Asp  
1 5 10 15  
Pro Met Thr Ile Cys Pro Pro Cys Met Cys Thr His Ser Cys Pro Pro  
20 25 30

Lys Gly Lys Pro  
35

<210> 591  
<211> 38  
<212> PRT  
<213> Conus aurisiacus

<400> 591  
Glx Lys Trp Leu Val His Ser Lys Ile Thr Tyr Cys Cys Gly Tyr Asn  
1 5 10 15  
Lys Met Asp Met Cys Pro Pro Cys Met Cys Thr Tyr Ser Cys Pro Pro  
20 25 30

Leu Lys Lys Lys Arg Pro  
35

<210> 592  
<211> 29  
<212> PRT  
<213> Conus aurisiacus

<400> 592  
Ala Pro Trp Thr Val Val Thr Ala Thr Thr Asn Cys Cys Gly Ile Thr  
1 5 10 15  
Gly Pro Gly Cys Leu Pro Cys Arg Cys Thr Gln Thr Cys  
20 25

<210> 593  
<211> 13  
<212> PRT  
<213> Conus geographus

<400> 593  
Glu Cys Cys His Pro Ala Cys Gly Lys His Tyr Ser Cys  
1 5 10

<210> 594  
<211> 13  
<212> PRT  
<213> Conus geographus

&lt;400&gt; 594

Glu Cys Cys Asn Pro Ala Cys Gly Arg His Phe Ser Cys  
 1 5 10

&lt;210&gt; 595

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus striatus

&lt;400&gt; 595

Ala Tyr Cys Cys His Pro Ala Cys Gly Pro Asn Tyr Ser Cys Gly Thr  
 1 5 10 15

Ser Cys Ser Arg Thr Leu  
 20

&lt;210&gt; 596

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Conus striatus

&lt;400&gt; 596

Ala Tyr Cys Cys His Pro Val Cys Gly Lys Asn Phe Asp Cys  
 1 5 10

&lt;210&gt; 597

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus rattus

&lt;400&gt; 597

Gly Cys Cys Cys Asn Pro Ala Cys Gly Pro Asn Tyr Gly Cys Gly Thr  
 1 5 10 15

Ser Cys Ser Arg Thr Leu  
 20

&lt;210&gt; 598

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus arenatus

&lt;400&gt; 598

Glx Asp Tyr Cys Cys Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu  
 1 5 10 15

Arg Cys Arg His Ile Arg  
 20

&lt;210&gt; 599

&lt;211&gt; 22

&lt;212&gt; PRT

&lt;213&gt; Conus eburneus

&lt;400&gt; 599

Glx Asp Tyr Cys Cys Thr Ile Pro Ser Cys Trp Asp Arg Tyr Lys Glu  
 1 5 10 15

Arg Cys Arg His Ile Arg  
 20

<210> 600  
 <211> 13  
 <212> PRT  
 <213> *Conus miles*

<400> 600  
 Asp Tyr Cys Cys His Arg Gly Pro Cys Met Val Trp Cys  
 1 5 10

<210> 601  
 <211> 13  
 <212> PRT  
 <213> *Conus jDedius*

<400> 601  
 Gly Cys Cys Ser Asp Pro Arg Cys Arg Tyr Arg Cys Arg  
 1 5 10

<210> 602  
 <211> 17  
 <212> PRT  
 <213> *Conus omaria*

<400> 602  
 Gly Cys Cys Ser His Pro Ala Cys Asn Val Asn Asn Pro His Ile Cys  
 1 5 10 15

Gly

<210> 603  
 <211> 17  
 <212> PRT  
 <213> *Conus omaria*

<400> 603  
 Gly Cys Cys Ser His Pro Ala Cys Asn Val Asn Asn Pro His Ile Cys  
 1 5 10 15

Gly

<210> 604  
 <211> 19  
 <212> PRT  
 <213> *Conus quercinus*

<400> 604  
 Glx Gly Cys Cys Ser Asp Pro Ala Cys Ala Val Ser Asn Pro Asp Ile  
 1 5 10 15

Cys Gly Gly

<210> 605  
 <211> 17  
 <212> PRT  
 <213> *Conus bandanus*

<400> 605  
 Pro Glu Cys Cys Thr His Pro Ala Cys His Val Ser His Pro Glu Leu  
 1 5 10 15

Cys

<210> 606  
 <211> 17  
 <212> PRT  
 <213> *Conus marmoreus*

<400> 606  
 Pro Glu Cys Cys Thr His Pro Ala Cys His Val Ser Asn Pro Glu Leu  
 1 5 10 15

Cys

<210> 607  
 <211> 15  
 <212> PRT  
 <213> *Conus miles*

<400> 607  
 Cys Cys Asn His Pro Ala Cys Ala Gly Lys Asn Ser Asp Leu Cys  
 1 5 10 15

<210> 608  
 <211> 16  
 <212> PRT  
 <213> *Conus magus*

<400> 608  
 Gly Cys Cys Tyr His Pro Thr Cys His Leu Glu His Ser Asn Leu Cys  
 1 5 10 15

<210> 609  
 <211> 17  
 <212> PRT  
 <213> *Conus nobilis*

<400> 609  
 Gly Cys Cys Glu Arg Pro Pro Cys Arg Trp Gln Asn Pro Asp Leu Cys  
 1 5 10 15

Gly

<210> 610  
 <211> 17  
 <212> PRT  
 <213> *Conus atlanticus*

<400> 610  
 Thr Cys Cys Ser Arg Pro Thr Cys Arg Met Glu Tyr Pro Glu Leu Cys  
 1 5 10 15

Gly

<210> 611  
 <211> 21  
 <212> PRT  
 <213> *Conus quercinus*

<400> 611

Asn Glu Cys Cys Asp Asn Pro Pro Cys Lys Ser Ser Asn Pro Asp Leu  
 1 5 10 15

Cys Asp Trp Arg Ser  
 20

<210> 612  
 <211> 16  
 <212> PRT  
 <213> Conus leopardus

<400> 612  
 Cys Cys Ser Asn Pro Ala Cys Asn Arg Tyr Asn Pro Ala Ile Cys Asp  
 1 5 10 15

<210> 613  
 <211> 17  
 <212> PRT  
 <213> Conus emaciatus

<400> 613  
 Asp Cys Cys Asn Phe Pro Ala Cys Ala Ala Ser Asn Pro Gly Leu Cys  
 1 5 10 15

Thr

<210> 614  
 <211> 14  
 <212> PRT  
 <213> Conus victor

<400> 614  
 Cys Cys Ser Ser Pro Pro Cys Phe Ala Ser Asn Pro Ala Cys  
 1 5 10

<210> 615  
 <211> 17  
 <212> PRT  
 <213> Conus cinereus gubba

<400> 615  
 Gly Gly Cys Cys Ser Phe Pro Pro Cys Ile Ala Asn Asn Pro Phe Cys  
 1 5 10 15

Ala

<210> 616  
 <211> 15  
 <212> PRT  
 <213> Conus flavidus

<400> 616  
 Gly Cys Cys Ser Asn Pro Pro Cys Ser Tyr Leu Asn Pro Ala Cys  
 1 5 10 15

<210> 617  
 <211> 16  
 <212> PRT  
 <213> Conus emaciatus



&lt;400&gt; 617

Asp	Cys	Cys	Ser	Asp	Pro	Pro	Cys	Ala	His	Asn	Asn	Pro	Asp	Cys	Arg
1				5					10					15	

&lt;210&gt; 618

&lt;211&gt; 17

&lt;212&gt; PRT

<213> *Conus generalis*

&lt;400&gt; 618

Gly	Cys	Cys	Ser	Asn	Pro	Pro	Cys	Tyr	Ala	Asn	Asn	Gln	Ala	Tyr	Cys
1				5					10					15	

Asn

&lt;210&gt; 619

&lt;211&gt; 25

&lt;212&gt; PRT

<213> *Conus wittigi*

&lt;400&gt; 619

Asp	Glu	Cys	Cys	Ala	His	Pro	Ser	Cys	Trp	Lys	Ala	Glu	Asp	Leu	Ile
1				5					10					15	

Cys	Thr	Asn	Gln	Arg	Arg	Arg	Thr	Leu
			20					25

&lt;210&gt; 620

&lt;211&gt; 20

&lt;212&gt; PRT

<213> *Conus characteristicus*

&lt;400&gt; 620

Gly	Cys	Cys	Ala	Ile	Arg	Glu	Cys	Arg	Leu	Gln	Asn	Ala	Ala	Tyr	Cys
1				5					10					15	

Gly	Gly	Ile	Ser
			20

&lt;210&gt; 621

&lt;211&gt; 19

&lt;212&gt; PRT

<213> *Conus betulinus*

&lt;400&gt; 621

Ser	Ala	Thr	Cys	Cys	Tyr	Tyr	Pro	Pro	Cys	Tyr	Glu	Ala	Tyr	Pro	Glu
1				5					10					15	

Ser Cys Leu

&lt;210&gt; 622

&lt;211&gt; 6

&lt;212&gt; PRT

<213> *Conus magus*

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(6)

&lt;223&gt; Xaa is gamma-carboxy-Glu

<400> 622  
Val Tyr Xaa Thr His Pro  
1 5

<210> 623  
<211> 14  
<212> PRT  
<213> Conus striatus

<400> 623  
Trp Ser Trp Arg Met Gly Asn Gly Asp Arg Arg Ser Asp Gln  
1 5 10

<210> 624  
<211> 11  
<212> PRT  
<213> Conus quercinus

<400> 624  
Asp Cys Gln Pro Cys Gly His Asn Val Cys Cys  
1 5 10

<210> 625  
<211> 29  
<212> PRT  
<213> Conus geographus

<220>  
<221> PEPTIDE  
<222> (1)..(29)  
<223> Xaa is gamma-carboxy-Glu

<400> 625  
Lys Phe Leu Ser Gly Gly Phe Lys Xaa Ile Val Cys His Arg Tyr Cys  
1 5 10 15

Ala Lys Gly Ile Ala Lys Glu Phe Cys Asn Cys Pro Asp  
20 25

<210> 626  
<211> 6  
<212> PRT  
<213> Conus magus

<400> 626  
Arg Pro Lys Asn Ser Trp  
1 5

<210> 627  
<211> 7  
<212> PRT  
<213> Conus magus

<220>  
<221> PEPTIDE  
<222> (1)..(7)  
<223> Xaa is hydroxy-Pro

<400> 627  
Ala Arg Xaa Lys Asn Ser Trp

1 5

<210> 628  
 <211> 6  
 <212> PRT  
 <213> Conus magus

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa is hydroxy-Pro

<400> 628  
 Arg Xaa Lys Asn Ser Trp  
 1 5

<210> 629  
 <211> 71  
 <212> PRT  
 <213> Conus geographus

<400> 629  
 Cys Cys Pro Ser Ser Lys Glu Asp Ser Leu Asn Cys Ile Glu Thr Met  
 1 5 10 15

Ala Thr Thr Ala Thr Cys Met Lys Ser Asn Lys Gly Glu Ile Tyr Ser  
 20 25 30

Tyr Ala Cys Gly Tyr Cys Gly Lys Lys Lys Glu Ser Cys Phe Gly Asp  
 35 40 45

Lys Lys Pro Val Thr Asp Tyr Gln Cys Gln Thr Arg Asn Ile Pro Asn  
 50 55 60

Pro Cys Gly Gly Ala Ala Leu  
 65 70

<210> 630  
 <211> 65  
 <212> PRT  
 <213> Conus geographus

<400> 630  
 Asp Glu Ser Lys Cys Asp Arg Cys Asn Cys Ala Glu Leu Arg Ser Ser  
 1 5 10 15

Arg Cys Thr Gln Ala Ile Phe Cys Leu Thr Pro Glu Leu Cys Thr Pro  
 20 25 30

Ser Ile Ser Cys Pro Thr Gly Glu Cys Arg Cys Thr Lys Phe His Gln  
 35 40 45

Ser Arg Cys Thr Arg Phe Val Glu Cys Val Pro Asn Lys Cys Arg Asp  
 50 55 60

Ala  
 65

<210> 631  
 <211> 60

&lt;212&gt; PRT

<213> *Conus geographus*

&lt;400&gt; 631

Asp	Asp	Ser	Tyr	Cys	Asp	Gly	Cys	Leu	Cys	Thr	Ile	Leu	Lys	Lys	Glu
1				5					10					15	

Thr	Cys	Thr	Ser	Thr	Met	Ser	Cys	Arg	Gly	Thr	Cys	Arg	Lys	Glu	Trp
			20					25					30		

Pro	Cys	Trp	Glu	Glu	Asp	Cys	Tyr	Cys	Thr	Glu	Ile	Gln	Gly	Gly	Ala
			35					40				45			

Cys	Val	Thr	Pro	Ser	Glu	Cys	Lys	Pro	Gly	Glu	Cys
	50					55					60

&lt;210&gt; 632

&lt;211&gt; 43

&lt;212&gt; PRT

<213> *Conus radiatus*

&lt;400&gt; 632

Gly	Cys	Val	Tyr	Glu	Gly	Ile	Glu	Tyr	Ser	Val	Gly	Glu	Thr	Tyr	Gln
1				5					10					15	

Ala	Asp	Cys	Asn	Thr	Cys	Arg	Cys	Asp	Gly	Phe	Asp	Leu	Ala	Thr	Cys
			20					25					30		

Thr	Val	Ala	Gly	Cys	Thr	Gly	Phe	Gly	Pro	Glu
		35				40				

&lt;210&gt; 633

&lt;211&gt; 86

&lt;212&gt; PRT

<213> *Conus striatus*

&lt;400&gt; 633

Ser	Gly	Pro	Ala	Asp	Cys	Cys	Arg	Met	Lys	Glu	Cys	Cys	Thr	Asp	Arg
1				5					10					15	

Val	Asn	Glu	Cys	Leu	Gln	Arg	Tyr	Ser	Gly	Arg	Glu	Asp	Lys	Phe	Val
			20					25					30		

Ser	Phe	Cys	Tyr	Gln	Glu	Ala	Thr	Val	Thr	Cys	Gly	Ser	Phe	Asn	Glu
		35					40					45			

Ile	Val	Gly	Cys	Cys	Tyr	Gly	Tyr	Gln	Met	Cys	Met	Ile	Arg	Val	Val
	50					55					60				

Lys	Pro	Asn	Ser	Leu	Ser	Gly	Ala	His	Glu	Ala	Cys	Lys	Thr	Val	Ser
65					70					75					80

Cys	Gly	Asn	Pro	Cys	Ala
				85	

&lt;210&gt; 634

&lt;211&gt; 24

&lt;212&gt; PRT

<213> *Conus purpurascens*

&lt;400&gt; 634

Asp Cys Cys Gly Val Lys Leu Glu Met Cys His Pro Cys Leu Cys Asp  
 1 5 10 15

Asn Ser Cys Lys Asn Tyr Gly Lys  
 20

&lt;210&gt; 635

&lt;211&gt; 36

&lt;212&gt; PRT

<213> *Conus geographus*

&lt;400&gt; 635

Gly Glu Pro Ile Pro Thr Thr Val Ile Asn Tyr Gly Glu Cys Cys Lys  
 1 5 10 15

Asp Pro Ser Cys Trp Val Lys Val Lys Asp Phe Gln Cys Pro Gly Ala  
 20 25 30

Ser Pro Pro Asn  
 35

&lt;210&gt; 636

&lt;211&gt; 16

&lt;212&gt; PRT

<213> *Conus generalis*

&lt;400&gt; 636

Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Pro Cys Cys Val Pro  
 1 5 10 15

&lt;210&gt; 637

&lt;211&gt; 20

&lt;212&gt; PRT

<213> *Conus tessulatus*

&lt;400&gt; 637

Asp Gly Cys Pro Pro His Pro Val Pro Gly Met His Lys Cys Met Cys  
 1 5 10 15

Thr Asn Thr Cys  
 20

&lt;210&gt; 638

&lt;211&gt; 84

&lt;212&gt; PRT

<213> *Conus radiatus*

&lt;400&gt; 638

His Pro Thr Lys Pro Cys Met Tyr Cys Ser Phe Gly Gln Cys Val Gly  
 1 5 10 15

Pro His Ile Cys Cys Gly Pro Thr Gly Cys Glu Met Gly Thr Ala Glu  
 20 25 30

Ala Asn Met Cys Ser Glu Glu Asp Glu Asp Pro Ile Pro Cys Gln Val  
 35 40 45

Phe Gly Ser Asp Cys Ala Leu Asn Asn Pro Asp Asn Ile His Gly His  
 50 55 60

Cys	Val	Ala	Asp	Gly	Ile	Cys	Cys	Val	Asp	Asp	Thr	Cys	Thr	Thr	His
65					70					75					80

Leu Gly Cys Leu